STIC-Biotech/ChemLib

117537

From:

Kaushal, Sumesh

Sent:

Tuesday, March 23, 2004 5:22 PM

r To:

STIC-Biotech/ChemLib

Subject:

09938391: Sequence and Interference Search

09/938,391 Sequence and Interference Search

Please search

SEQ ID NO:2

PRT 230

SEQ ID NO:4

PRT 184

SEQ ID NO:1

DNA 829

SEQ ID NO:3

DNA 555

thanks

S. Kaushal

AU1636, REM2.B85 Ph: 571-27-20769

Mail Box: REM2.C70

Interference Sarch files semoved - 8h

Searcher: ______Phone: _______
Location: ______
Daté Picked Up: ________
Date Completed: _________
Searcher Prep/Review: _______
Clerical: _______
Online time: _______

TYPE OF SEARCH:

NA Sequences:

AA Sequences:

Structures:

Bibliographic:

Litigation:

Full text:

Patent Family:

Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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March 29, 2004, 09:11:19 ; Search time 3335.77 Seconds
    (without alignments)
    10771.549 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

Summaries ID Description	A3399629 Sequence A339629 Sequence A339629 Sequence A339629 Sequence A339629 Sequence A339629 Sequence A339629 Sequence A3399629 Sequence	BD188110 BD188110	AA599051 BD100111 BD1188111	BD240900 Expre	BC033715 HOMO	AK130835 AK130835	AF018082 ACMO AF018081 HOMO	AK098216 AK098216 Homo	IS1045 Sequence	AX409531	AX370851 Sequence	U03714	D17546 Mus 1	IS1044 Seque	L22545 Mouse	AF416592 HOMS AR431862 SECT	AX81610	AR193165 Seq.	AX100086 Sequence	BD26674	AX39566Z Seque	BD08140	AF282883 Homo	AKBIBIUS AFIBADED F	AR19316	AX100099	AX370853 Sequence	BD272245	AA084408	AR183471 Sequence	AR183520 AB217279	AR282751	6 AX042272 Sequence 6 AX490666 Sequence	ALIGNMENTS	829 bp DNA linear PAT 06-JUN-200 cent BP1191036.	35409	(dog)	, Chordata, Craniata, Vertebrata, Euteleostomi; , Carnivora, Fissipedia, Canidae, Canis.	
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Shepard, M.G. and Tong, \mathcal{L} / \mathcal{M}, Method and composition for diagnosing and treating diseases
Method and composition for diagnosing and treating diseases relating to anglogenesis.
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Patent: JP 200300268-A 1 07-JAN-2003;
PFIZER PRODUCTS INC
OS Canis sp. (dog)
PN JP 2003000268-A/1
PD 07-JAN-2003
PF 24-AUG-2001 JP 2001254697
PR 25-AUG-2000 US 60/227924
PI MICHALL GEORGE SHEPPARD, XIAO TONG
PC C12N15/09,A01K67/027,A61K31/7088,A6
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100.0%; Score 829; DB 6
Best Local Similarity 100.0%; Pred. No. 1e-99;
Matches 829; Conservative 0; Mismatches
                                                                                                                                                                                        /organism="Canis familiaris"
/mol_type="unassigned DNA"
/db_xref="taxon:9615"
                                                                       EP 1191036-A 1 27-MAR-2002;
roducts Inc. (US)
Location/Qualifiers
                                                                          Patent: EP 1191036-1
Pfizer Products Inc
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/organism='Canis sp. (dog)'

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Best Local Similarity 100.0%; Score 829; DB 6; Length 829;
Best Local Similarity 100.0%; Pred. No. 1e-99;
Matches 829; Conservative 0; Mismatches 0; Indels
1. .829
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/mol_type="genomic DNA"
/db_xref="taxon:9616"
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Dp 90	241 CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGGCCCGCATC 300
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ò	619 GAGGCCGCGAGCCGCCACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGAC 678
Dp qu	481 GAGGCGGGAGCTGCGCCCACGCCTTCGTGCTCTGCATCGAGAACAGCGTCATGACC 540
λo	679 TCCTTCTCCAAGTAG 693
Db du	541 rccrrcrccaAgrag 555
RESULT 4 BD188111 LOCUS	11
DEFINITION	Omposition tot dragmosing and creating areas angiogenesis.
ACCESSION VERSION KEYWORDS	BD188111 BD188111.1 GT:32997850 JP 200300268-A/2.
SOURCE	
1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	CONTROL OF THE PROPERTY OF THE
TITLE	Sueppara, m.c. and rougher. Method and composition for diagnosing and treating diseases
JOURNAL	Patent: UP 2003000268-A 2 07-JAN-2003;
COMMENT	PFIZER FROUNCIS INC. OS Canies Sp. (409) NY IT JAARAGESA/2
	PD 07-2003000200-7/2
	24-AUG-2001 UF 2001234037 25-AUG-2000 US 60/227924
	PI MICHAEL GEORGE SHEPPARD,XIAO TONG PC C12N15/09,A01K67/027,A61K31/7088,A61K35/76,A61K39/395 PC
	, A61K39/395, A61K45/00, PC A61K48/00, A61P7/00, A61P9/00, A61P9/10, A61P15/00, A61P17/00, PC
	A61P17/02, PC A61P17/06, A61P19/02, A61P19/08, A61P25/00, A61P27/02, A61P27/06,
	PC A61P29/00, PC A61P31/00,A61P35/00,A61P35/02,A61P35/04,A61P37/06,A61P43/00,
	PC C07K14/47, PC C07K16/18, C07K19/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC
	1/02,G01N33/15, 301N33/50,C12N15/00,C12N5/00
	CC CANINE ENDOSTATIN NUCLEOTIDE SEQUENCE FH Key Location/Qualifiers
	FT source 1555 FT Source /organism='Canis sp. (dog)'.
FEATURES	Location/Qualifiers
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	/mol_type="genomic DNA" /dh xref="taxon:9616"

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BC033715
Homo sapiens, Similar to collagen, type XVIII, alpha 1, clone IMAGE:4425380, mRNA, partial cds.
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2637)
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        Location/Qualifiers
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99.8%; Pred. No. 4.1e-63;
iive 0; Mismatches 1
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/organism="Canis familiaris"
/mol type="genomic DNA"
/db_xref="taxon:9615"
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Location/Qualifiers
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AUTHORS
TITLE
JOURNAL
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Eukaryota; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

I (bases 1 to 552)

Expression and export of angiogenesis inhibitors as immunofusins of tent: UP 200253036-A 20 30-UUL-2002;

Expression and export of angiogenesis inhibitors as immunofusins of tent: UP 200253036-A/20

Patent: UP 2002533036-A/20

PN JP 200253036-A/20

PN JP 2002533036-A/20

PN JP 200253036-A/20

PN JP 2002533036-A/20

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PN JP 20
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Query Match 66.9%; Score 555; DB 6; Length 555; Best Local Similarity 100.0%; Pred. No. 1e-63; Matches 555; Conservative. 0; Mismatches 0; Indels
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COMMENT

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AK130835
Homo sapiens CDNA FLJZ7325 fis, clone TMS08226, highly similar to collagen alpha I(XVIII) chain precursor.

AK130835.1 GI:34527728
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Unpublished
2 (bases 1 to 1388)
Sugano, S. and Suzuki, Y.
Direct Submission
Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T.,
Irle,R., Otsuki,T., Sato,H., Nishikawa,T., Nagai,K., Isogai,T.
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Homo sapiens (human)
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc.mgc@nhgri.nih.gov/

Contact: nisc.mgc@nhgri.nih.gov/

Contact: nisc.mgc@nhgri.nih.gov/

Contact: N. Benjamin.B.,

Blakesley.R.W. Bouffard.G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi.P.,

Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric.P., Legaspi.R.,

Maduro,Q.L., Masiello,C., Maskeri.B., Mastrian,S.D.,McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,B.D.
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/product="Similar to collagen, type XVIII, alpha 1"
/db xref="all:1217018149"
/db xref="all:21708149"
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/organism="Homo sapiens"

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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Tisaue Procurement: ATC
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.larity 77.7%; Pred. No. 2.4e-57;
Conservative 0; Mismatches 152;
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NEDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; J' -end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute. 953 AAGCCCGGGGCACGCATCTTCTCCTTTGACGGCAAGGACGTCCTGAGGCACCCCACGGG 1012 1132 1013 CCCCAGAAGAGGGGTGTGGCATGGCTCGGACCCCAACGGGCGCCAGGCTGACCGAGGAGCTAC 1072 1133 édékédétreérédedékékendedededekendedarokadonakarokatondenden 1192 1193 GAGAACAGCTTCATGACTGCCTCCAAGTAGCCACCGCCTGGATGCGGATGGCCGGAGAGG 1252 604 CCCGGGGCCCCGCACCACGGCTCCTACGTGCACTTCCAGCCGGCTCGCCCCACTGGTGGG 120 099 180 712 240 772 300 832 360 892 420 952 480 540 900 660 720 University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flodmaeims:u-tokyo.ac.jp, Tel:81-3-5449-5286, Pax:81-3-5449-5416) 9 1 CCCTGGCGGCCAGATGACATCCTGGCCGCCCCCGCGCCTGCTGGACCCCCAGCCCTAC -----CCACCCGCCCACAGCCACGCGCGACTTCCAGCCGGTGCTCCACCTGGTTGCG 181 CTGAACAGCCCGCAGCCGGCGATGCGAGGCATCCGGGGAGCGGAGCTTCCAGTGCTTC 713 CTCAACAGCCCCCTGTCAGGGGGCATGCGGGGGCATCCGCGGGGCCGACTTCCAGTGCTTC CAGCAGGCGCGCGCGGGGGCTGGCCGGCACCTTCCGGGGCCTTCCTGTCGTCGCGGCTG 773 cháchádcádadccándadaradadadadatracacacarracharachadadada 833 CAGGACCTGTACAGCATCGTGCCGTGCCCACCGCGCAGCCGTCGCCATCGTCAACCTC 361 AGGGACGAGGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCCAGCTG 893 AAGGACGAGCTGTTTCCCAGCTGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTG AAGCCCGGGGCCCGCATCTTCTTTTCGACGGCAGATGTCCTGCAGCACCCCGCCTGG 481 CCCCGGAAGAGGGTGTGGCACGGCTCCGACCCCCAGCGGCGCCGCCTGACCGACAGCTAC 541 TGCGAGACGTGGCGGACGGAGGCCCCGGCGGCCACCGGGCAGGCGTCGTGCTGCTGGCG 1073 reneadaderecenceadecrecercescencescencescencercercereces 601 GGCAGGCTGCTGGAGCAGAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATC GAGAACAGCGTCATGACCTCCTTCTCCAAGTAGGGCCGCGCGCCCCACGGACAGGCGGGG 301 CAGGACCTCTACAGCATCGTGCGCCGCCGCCGACCGCACCGGGGTGCCCGTCGTCAACCTC Query Match 60.7%; Score 503.2; DB 9; Length 1388; Best Local Similarity 77.6%; Pred. No. 4.8e-57; Matches 664; Conservative 0; Mismatches 153; Indels 39; Gaps 61 199 241 421 661 FEATURES COMMENT ORIGIN В 상염 8 8 ò g à g ò Dp δ В ઠ d à В 6 g 8 g

Qy 7	721 GAGGGGGCGCCGCAGGAGCATCCGCCGGGG756
Db 12	253 ACCGGCGGCTCGGAGGAGGCCCCACCGTGGGCAGGGAGGG
	GGGCCTGGCCGGACGCTTGCCTGCACG-TCACGTTTAATGTAATCCTCAAGAAATA 813
er e	isis Cadsaccidscrecrairentrecidialadricaegriicaigraficenaraara 1372 814 AAAGGAAGCCAAAGAG 829
	AAAGGAAGCCAAAGAG 13
APO18082 LOCUS DEFINITION ACCESSION VERMODE	AF018082 5408 bp mRNA linear PRI 18-MAR-1998 GOL1841) mRNA, alternatively spliced, short form, complete cds. AF018082 AF018082. GI:2920536
SOURCE ORGANISM	omo sag omo sag ukaryot ammalia
REFERENCE AUTHORS TITLE	<pre>gpa,R., Rehn,M., Purmo ppa,R., Rehn,M., Purmo iructure of two varian sepecific differences</pre>
JOURNAL MEDLINE PITRMED	COLLESPONALING LEALBOOK NO. (1998) MARINIX Biol, 16 (6), 319-328 (1998) 98164096
	2 (bases 1 to 5408) Saarela, Ylikarppa, R., Rehn, M., Purmonen, S. and Pihlajaniemi, T.
	Direct Summission Submitted (28-UTL-1997) Dept. of Medical Biochemistry, University of Onlu. Kalaninite 52 A. Oulu 90220. Finland
FEATURES SOURCE	ocation/Qualifiers
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	TABLEY N.V.P.G.*GFTH.COBBUDGETHE COLLEGE COLLOGATION TO PEPAYTER PROGRAM EPPROGRAM EPP
	QGPPGPPGPSFKHDKLTFIDMEGSGFGGDLEALRGPRGFPGPPGPPGPPGPPGPPGFPGFPGFPGFPGFPGFPGFPG
	NOSNOARFGEROKKOSSGLANDEGEROKEET OF FOF TO GOT STATEN STATE
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	TARRED FOR THE VALUE OF THE CONTRACT OF THE CO

RPTSPPAHSHRDFQPVLHLVALNSPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLS SRLQDLYSTVRRADRAAVPLVNLKDELLFPSWEALFSGSBGPLKPGARIFSPDGKDVL RHPTWPQKSVWHGSDPNGRRLTESYCETWRTEAPSATGQASSLLGGRLLGGSAASCHH AYIVLCIENSPWIASK"

4160 3860 caddacciddccaracrirccidraracricacdrircardrarccrcaadaara 4220 3452 3508 3620 3680 3740 3920 3981 decadectroridedecada arecododa do recontración de contracación de contrac 4100 м , 360 3741 AAGGACGAGCTGCTGTTTCCCAGCTGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTG 3800 480 540 9 813 600 720 240 420 180 09 3393 CCCTGGGGGGGAGATGACATCCTGGCCAGCCCCCCCCGCCGGCCCGAGCCCAAC 661 GAGAACAGCGTCATGACCTCCTTCTCCAAGTAGGGCCGCGCGCCCACGGACAGGCGGGG CCCCGGAAGAGCGTGTGGCACGGCTCCGACCCCAGCGGCGCCCCCCTGACCGACAGCTAC TGCGAGACGTGGCGGACGGCCCCCGGCCACCGGGCAGGCGTCGTCGCTGGCG 601 GGCAGGCTGCTGGAGCAGGAGCCGCGAGCTGCCACGCCTTCGTGGTGCTCTGCATC 4041 GAGAACAGCTTCATGACTGCCTCCAAGTAGCCACGGCTGGATGCGGATGGCCGGAGAG -- GGGCCTGGCCGGGGACGCTTGCCTGCACCG-TCACGTTTAATGTAATCCTCAAGAAATA CCCTGGCGGCCAGATGACATCCTGGCCGGCCCCCCCGCGCCTGCTGGACCCCCAGCCCTAC CCCGTCCACACCCACCCACCCACCAGCACTTCCAGCTGGTGCTGCACCTGGTGGCTGCTGCTGGTGGTCGCCC CTGAACAGCCCGCAGCCGGCCATGCGAGGCATCCGGGGAGCGGACTTCCAGTGCTTC 3561 crchacadeceeeroreadadadadadadadadadadadadadadadaradara 361 AGGACGAGGIGCICITCCCCAGCIGGAGGCCTTAITCICGGGCTCCGAGGGCCTG AAGCCCGGGGCCCCCCATCTTCTCTTTTCGACGGCAGATGTCCTGCAGCACCCCCGCCTGG 4101 Accédedecricada ada adececida esta de adocado esta acedece adececento esta a acede adecemento de acede adecemento de acede a acede adecemento de acede acede acede a acede aced Gaps 39; Length 5408 Query Match 60.7%; Score 503.2; DB 9; Length Best Local Similarity 77.6%; Pred. No. 3.2e-57; Matches 664; Conservative 0; Mismatches 153; Indels 721 GAGGGGGGCCCCGCAGGAGCATCCGCCGCCCCGGGG-AAAGGAAGCCAAAGAG 4236 AAAGGAAGCCAAAGAG 829 4161 814 4221 541 301 421 757 3453 121 3509 181 241 481 ORIGIN g g g ò 원 ઠે à 임 ò ద ď ò g δ ਨੇ d g d ò 엄 à ò ઠે g à ò d à $\stackrel{>}{\circ}$

RESULT 9 AF018081

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/ note = "alternatively spliced; long form (NC1-493)"

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Homo sapiens type XVIII collagen (COL18A1) mRNA, alternatively
AP018081
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 522)
Saarela, J., Ylikarppa, R., Rehn, M., Purmonen, S. and Pihlajaniemi, T.
Complete primary structure of two variant forms of human type XVIII
collagen and tissue-specific differences in the expression of the
Matrix Biol. 16 (6), 319-328 (1998)
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Submitted (28-JUL-1997) Dept. of Medical Biochemistry, University of Oulu, Kajaanintie 52 A, Oulu 90220, Finland
Location/Qualifiers
1. 5929
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ilarity 77.6%; Pred. No. 3.1e-57;
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1. .5929
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3974 CCGGGACCCCGCACACCTCCTACGTGCACCTGGGGCGGCGACACAAG---- 4029

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61 CCCGGGGCCCCCACCACGCTCCTACGTGCACTTCCAGCCGGCTCGCCCCACTGGTGGG 120

4030 -----CCCACCCACCCACCCACCGCGACTTCCAGCCGGTGCTCCACCTGGTTGCG 4081

121 CCCGTCCACACCCACACACACACACACACAGACTTCCAGCTGGTGGTGCTGCACCTGGTGGCT

4082 circhachachachachachachiadaaachidaaaachidaahaircaanachida 4141

181 CTGAACAGCCCGCAGCCGGCCGTGCGAGGCATCCGGGGAGCGGACTTCCAGTGCTTC 240

1142 CAGCAGGGGGGGGGGGGGGGGGGGGGGGCTTCCGGGGCTTCCTGGGGCCTG

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361 AGGGACGAGGTGCTCTCCCCAGCTGGGAGGCCTTATTCTCGGGGCTCCGAGGCGAGGCTG 4262 Aaddacdacriciriricccacricadaddcricricricaddcricricaddric 421 AAGCCCGGGGCCCGCATCTTCTTTTCGACGGCAGAGATGTCCTGCAGCACCCCGCCTGG

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4382 CCCCAGAAGAGCGTGTGGCATGGCTCGGACCCCAACGGGCGCAGGCTGACCGAGAGACTAC 4441

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CCCCGGAAGAGCGTGTGGCACGGCTCCGACCCCAGCGGCGCCCCTGACCGACAGCTAC 540

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4501 4502 GGCAGGCTCCTGGGGCAGAGTGCCGCGAGCTGCCATCACGCCTACATCGTGCTCTGCATT 4561 4682 CAGGACCTGGCTGCATACTTTCCTGTATAGTTCACGTTTCATGTAATCCTCAAGAAATA 4741 9 1562 GAGAACAGCTICATGACTGCCTCCAAGTAGCCACCGCCTGGATGCGGATGGCCGGAGAGG 4621 720 4442 ferenciació de de desercidade en contrador de desercidades de defensiva de desercidades de desercidades de desercidades de desercidades de desercidades de defensiva de desercidades de desercidades de defensiva de desercidades de dese 601 GGCAGGCTGCTGGAGCAGGAGGCGGGGGGCTGCCGCCACGCCTTCGTGGTGCTCTGCATC 661 GAGAACAGCGTCATGACCTCCTTCTCCAAGTAGGGCCGCGCGGCCCACGGACAGGCGGGG 757 -- GGGCCTGGCCGGGACGCTTGCCTGCACG-TCACGTTTAATGTAATCCTCAAGAAATA 721 GAGGGGGCGCCCCCAGGAGCATCCGCCGCCCCCGGGG-----814 AAAGGAAGCCAAAGAG 829

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AANUBEZIG TONA FLJ40897 fis, clone UTERUZ002964, highly similar AKO99216 RESULT 10 AK098216 LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS

4742 AAAGGAAGCCAAAGAG 4757

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AK096216.1 GI:21758185 oligo capping; fis (full insert sequence). Homo sapiens (human) Homo sapiens

Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K., Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R., REFERENCE AUTHORS

Submitted (04-UUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (Email-genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-418-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Blotechnology (RAB); CDNA library of construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Blotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB, annotation: HRI and RAB. Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Satto,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanebori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and /mol_type="mRNA"
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60.5%; Score 501.6; DB 9; Length 2364; 77.5%; Pred. No. 6.7e-57; Live 0; Mismatches 154; Indels 39; 663; Conservative Best Local Similarity Query Match Matches

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1578 cccqqqqccccccccccacaccrccracgraccrccracacccrccacacaccacacac--- 1633 1518 cccradcacadaraacarccradccadcccccrcaccradcccaagcccrad 1577 CCCGGGGCCCCGCACCACGGCTCCTACGTGCACTTCCAGCCGGCTCGCCCCACTGGTGGG 120 1 CCCTGGCGGGGAGATGACATCCTGGCCGGCCCCCCGGCGCCTGCTGGACCCCCAGCCCTAC 60 61 οp g

1746 CAGCAGGCGGGGCCGTGGGGCTGGCGGCCTTCCGCGCCTTCCTGTCCTGGCGCCTG 1805 1806 CAGGACCTGTACAGCATCGTGCGCCGTGCCGACCGCGCACCCTGCCCATCGTCAACCTC 1865 ઠે ò 셤

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AGGGACGAGGTGCTCTTCCCCAGCTGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTG	Qy 481 CCCCGGAAAGCGTGTGGCACGCCCCCGACGGGGCCCGCCGACACACGGGGCCCGACACACACGGGCGCACACACACGACG	Oy 601 GGCAGGCTGCTGGAGCAGGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATC 660 Db 1966 GGCAGGCTCCTGGGGAGTGCCGCGAGCTGCCATCACGCTACATCGTGCTTCTGCATT 2025	GAGAACAGCTTCATGACTCCTCCAAGTAGCCACCGCCTGGATGCAGATGGCCGGGGGGGG	Db 2086 ACCGGGGGGCTCGGAGGAGGCCCCACGTGGGCGAGCAGCGGGCCGGGCCCTGGGCCC 2145 Qy 757GGGCCGGGGGGGGGCTTGCCTGCACCG-TCACGTTTAATGTAATCCTCAAGAAATA 813 Db 2146 CAGGACCTGGCCGTACTTTCCTGTATAGTTCATGTAATCCTCAAGAAATA 2205	Qy 814 AAAGGAAGCCAAAGAG 829 	RESULT 12 AX409531 LOCUS LOCUS DEFINITION Sequence 2178 from Patent W00229103. ACCESSION AX409531. GI:21442236	KEYWOKUS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Alvares, Gene exp Patent: GENE LOG	FEATURES Location/Qualifiers 1.3394 /organiam="Homo sapiens" /mol_type="unassigned DNA"	<pre>xon:9606" GenBank Accession No. L22548"</pre>	Gaps		Qy 61 CCCGGGGCCCCGCACCACGGCTCCTACGTGCACCTGCGGCTCGCCCCACTGGTGGG 120
Qy 541 TGCGAGACGTGGCGGACGGAGGCCCCCGGCGGCCACCGGGCAGGCGTCGTCGCTGCTGGCG 600 Db 2046 TGTGACACGTGGCGAAGGAAGGCTCCCTCGGCCACGGGCCACGGCCTCCTCGTGGGG 2105 Qy 601 GGCAGGCTGCAGGAGGCCGCGAGCTGCCGCCACGCTTCGTGGTGTCTGTGATGCTTGTGTGTG	Qy 661 GAGAACAGCGTCATGACCTCCTTCTCCAAGTAGGGCGGGGGGGG	757GGGCCTGGCCGGGACGC 		RESULT 11 15.1045 LOCUS 15.1045 LOCUS Sequence 4 from patent US 5643783. ACCESSION 15.1045 VERSION 15.1045.1 GI:2472748	_	AUTHORS Olsen, B.R. and Oh, S.P. TITLE Collagen and uses therefor JOHENAL Patent: US 5443783-4 01-ULL-1997, FEATURES Location/Qualifiers source	ORIGIN Query Match 59.9%; Score 496.8; DB 6; Length 3394; Bost Local Similarity 77.1%; Pred. No. 2.5e-56; Matches 660; Conservative 0; Mismatches 157; Indels 39; Gaps 3;	Oy 1 CCCTGGCGGCAGATGACATCCTGGCCGCCCCCGGGCCTGCTGGACCCCCAGCCCTAC 60	QY 61 CCCGGGGCCCGCACCACGGCTCCTACGTGCACTTCCAGCCGGCTCGCCCACTGGTGGG 120	QY 121 CCCGTCCACACCACACCCACACCCACACTTCCAGCTGCTGCTGCTGCTGGTGGTGGT 1494	Qy 181 CTGAACAGCCGGAGCGGCGGCGATCCGAGGAACGGAACTTCCAGTGCTTC 240 Db 1546 CTCAACAGCCCCTGTCAGGGGGCATCCGCGGGCCGACTTCCAGTGCTTC 1605	Oy 241 CAGCAGGGGGGGGGGGGGGGGGGCACCTTCCGGGCCTTCCTGTCGTGGCGGCTG 300	Qy 301 CAGGACCTCTACAGCATGGGCGCGGCGGCGCGCGGGGGGGG

2085 AAGGACGAGCTGCTTTCCCACCTGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTG 1785 1845 1905 1965 2025 2145 1605 CAGGACCTGTACAGCATCGTGCGCGTGCCGACCGCGCAGCGTGCCTTCGTCAACCTC 1725 2146 caddacciddcigccaracifrictidraracificacdifficardraafccfdagaara 2205 540 300 420 480 909 999 720 CAGGACCTCTACAGCATCGTGCGCCGCGCCGACCGCACCGGGGTGCCCGTCGTCAACCTC 360 CCCGTCCACACCCACACCCCACACCACCAGGACTTCCAGCTGGTGCTGCACCTGGTGGCC 180 GOCAGOCTCCTGGGGCAGAGGCGGGGGCTGCCATCACGCCTACATCGTGCTCTGCATT GAGAACAGCGTCATGACCTCCTTCTCCAAGTAGGGCCGCGCGCCCACGGACAGGCGGGG 2086 Accelectectedadadecceleacedadecadecadecadecadecadeceredece 757 --GGGCCTGGCCGGGACGCTTGCCTGCACCG-TCACGTTTAATGTAATCCTCAAGAAATA crcaacaccccretrcaeeceecareceeecearcceeeeceeceeccarccaerectrc CCCCGGAAGAGGGGTGTGGCACGGCTCCGACCCCAGCGGGCGCCCCTGACCGACAGCTAC TGCGAGACGTGGCGGACGGACGGCCCCGGCGACCGAGGCGTCGTCGCTGCTGGCG GCCAGGCTGCTGGAGCAGGAGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATC 2026 gagaacagerricargaetreeerecaagragecaeceeeregargeagargecegaaga GAGGGGCGCCCGCAGGAGCATCCGCCGCCCCGGGG--------Aeggaceaegrecrerrececaegregeaegecerrarrereegecreeaegeceaegree AAGCCCGGGGCCCGCATCTTCTTTTCGACGGCAGAGATGTCCTGCAGCACCCCCGCTTGG CTGAACAGCCCGCAGCCGCCATGCGAGGCATCCGGGGAGCGGACTTCCAGTGCTTC CAGCAGGCGCGCGCGCGCGCGCCGGCACCTTCCGGGCCTTCCTGTCGTCGTCGCGGCTG 2206 AAAGGAAGCCAAAGAG 2221 AAAGGAAGCCAAAGAG 829 814 541 1966 1546 1606 301 1726 1786 1846 1906 121 1666 361 421 601 661 721 1494 181 241 481 중 음 음 g ò ò g ö ∂ ద ò g 8 g 강 쉽 ò 셤 ò a S 8 δ q

RESULT 13 HUMCOL18AX

HUMCOL18AX 3394 bp mRNA linear PRI 01-NOV-1994 Human collagen type XVIII alpha 1 (COL18A1) mRNA, partial cds. L22548 L22548.1 GI:348908 alpha-1 type XVIII collagen. Homo sapiens (human) Homo sapiens LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Mammalia: Butheria; Primates; Craniata; Vertebrata; Euteleostomi; Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3394)

10h.S.P., Warman, M.L., Seldin, M.F., Cheng, S.D., Knoll, J.H.,

17mmons, S. and Olsen, B.R.

Cloning of cDNA and genomic DNA encoding human type XVIII collagen and localization of the alpha 1(XVIII) collagen gene to mouse chromosome 10 and human chromosome 21

Genomics 19 (3), 494-499 (1994)

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TITLE

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AAGGACGAGCTGCTTTCCCAGCTGGGAAGCTCTGTTCTCAGGCTCTGAGGGTCGGCTG

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421 AAGCCCCGGGATCTTCTTTCGACGGCAGATGTCCTGCAGCACCCCGGCTGG

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JOURNAL MEDLINE PUBMED

1545 1605 1665 1725 1437 1493 360 180 300 420 9 181 CTGAACAGCCCGCAGCCGGGCGATGCGAGGCATCCGGGGAGCGGACTTCCAGTGCTTC 1546 CTCAACAGCCCCCTGTCAGGGGGCTTCCGGGGGCGACTTCCAGTGCTTC съесъесесесесесесествессесьстиссвяестиствистеств cascascacceresservescesescarescesescerescescerescenteriorical CAGGACCTCTACAGCATCGTGCGCCGCCGACCGCACCGGGGGTGCCCGTCGTCAACCTC 361 AGGGACGAGGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTG Gaps 59.9%; Score 496.8; DB 9; Length 3394; 77.1%; Pred. No. 2.5e-56; Live 0; Mismatches 157; Indels 39; /codon_start=1 /product="collagen type XVIII alpha 1" /protein id="AAA51864 1" /db_xref="GI:562794" CDNA /organism="Homo sapiens" /mol_type="mxNA" /db_xref="taxon:9606" /map="11q22.3" /tissue_type="liver" source text: Homo sapiens Location/Qualifiers /dev_stage="adult" L. 3394 /gene="COL18A1" gene="COL18A1" 1. .2055 Matches 660; Conservative Query Match Best Local Similarity Original 1494 241 1606 1666 61 301 gene COMMENT CDS ORIGIN 요 ద g ઠે 셤 ठे ò 셤 8 g ò ò

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1. 1449 /standard_name="COL18A1" GAGAACAGCGTCATGACCTCCTTC 684 Location/Qualifiers U03714.1 GI:487733 8188673 661 481 619 VERSION KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL RESULT 15 MMU03714 LOCUS ACCESSION FEATURES CDS ठे 8 8 8 ò g õ 유 ઠે ద ઠે 셤 1966 GGCAGGCTCCTGGGGCAGAGTGCCGCAGGTGCCATCACGCCTACATCGTGCTCTGCATT 2025 2026 gagaacagerreargaetrgeerrecaagrageeacegeerggargeargeeggagagagg 2085 2086 Accedececredadedececedades 2145 2146 CAGGACCTGGCTGCATACTTTCCTGTATAGTTCACGTTTCATGTAATCCTCAAGAATA 2205 PAT 01-MAR-2002 211 CCCTGGCGGGCAGATGATGATCCTGGCCAGCCCCCTCGCCTGCCCGGGCCCCAGCCCTAC 270 121 cccerccacacccacacccacacccacacacacarccaacaracaracaracaracaracaracaracaracaracaracaracaca 180 CAGCAGGCGCGGGCCGTGGGGGCTGGCGAGCCTTCCGCGCCTTCCTGTCTCTGCGCGCCTG 498 CTGAACAGCCCGCAGCCGGCCATGCGAGCCATCCGGGGAGCGGACTTCCAGTGCTTC 240 CAGGACCICTACAGCATCGTGCGCCGCCGGACCGCACCGGGGTGCCCGTCGTCAACCTC 360 720 1 CCCTGGCGGGCAGATGACATCCTGGCCGGCCCCCCGCGCCTGCTGGACCCCCAGCCCTAC 60 1. .900 /organism="synthetic construct" /mol type="unassigned DNA" /db.xref="taxon:32630" /note="maxA for mIgSP fused to COL18A1 exons 38-41 for pEnd-HR#1" GGCAGGCTGCTGCAGGAGGCGGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATC GAGAACAGCGTCATGACCTCCTTCTCCAAGTAGGGCCGCGCGCCCCACGGACAGGCGGGG --GGGCCTGGCCGGGACGCTTGCCTGCACCG-TCACGTTTAATGTAATCCTCAAGAAATA 12; Gaps Query Match
59.5%; Score 493.2; DB 6; Length 900;
Best Local Similarity 83.9%; Pred. No. 1.1e-55;
Matches 574; Conservative 0; Mismatches 98; Indels 12 linear 721 GAGGGGGGCCCCGCAGGAGCATCCGCCGCGCCCCGGGG------Chapman, P.W., de Luca, G. and Falciola, L. Method of producing functional protein domains Patent: WO 0210372-A 12 07-FEB-2002; Applied Research Systems ARS Holding S.A. (AN) Location/Qualifiers AX370851 Squence 12 from Patent W00210372. AX370851 AX370851.1 GI:19168980 2206 AAAGGAAGCCAAAGAG 2221 AAAGGAAGCCAAAGAG 829 synthetic construct synthetic construct artificial sequences. 271 241 61 327 181 379 439 601 199 757 814 RESULT 14
AX370851
LOCUS
DEFINITION
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VERSION
KEYWORDS ORGANISM AUTHORS JOURNAL REFERENCE FEATURES ORIGIN

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1615 bp mRNA linear ROD 13-AUG-1994 Mus musculus BALB/c alpha 1 type XVIII collagen (COL18A1) mRNA, partial cds. U03714
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Rehn,M.V.
Plrect Submission
Submitted (24-NOV-1993) Marko Rehn, Department of Medical
Biochemistry, University of Oulu, Kajaanintie 52 A Fin-90220, Oulu,
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Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Primary structure of the alpha 1 chain of mouse type XVIII

collagen, partial structure of the corresponding gene, and
comparison of the alpha 1 (XVIII) chain with its homologue, the
alpha 1(XV) collagen chain
J. Biol. Chem. 269 (19), 13929-13935 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619 AAGCCCGGGGGACGCATCTTCTTTCACGCCAAGGACGTCCTGAGGCACCCCACCTGG
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QPGARIFSPGGWDVLRHPAMPQKSVWHGSDPSGSRLMESYCETWRTETTGATGQASSL
LSGRLLEQKAASCHNSYIVLCIENSFWISFSK"
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1414 ATTGAGAATAGCTTCATGACCTCTTTCTCCAATAGGGCCTCTGCCAGCTAGGGTGCAG 1473

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March 29, 2004, 09:08:09; Search time 369.576 Seconds (without alignments) 9529.183 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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An isolated nucleic acid molecule for the treatment of angiogenesis-

WPI; 2002-354068/39. P-PSDB; AAO17429.

	Aax35375 SEQ ID 50	Aaa68203 Human end	Aac62023 Nucleotid		Abk50685 cDNA enco		-							_	Abk09978 Synthetic		Aac67777 Murine en	Abk47719 cDNA enco	Aax58740 DNA encod	Aaz08748 Mouse end		Aad18701 Mouse end
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ALIGNMENTS

RESULT 1

Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; angiofibroma; wound granulation; coronary collateral; collateral; arteriovenous malformation; collateral; acteriovenous malformation; ischaemic limb angiogenesis; diabetic neovascularisation; fracture; coronary collateral; antipsoriatic; antidiabetic; ophthalmological; /*tag= a /product= "pro-endostatin" /partial /note= "no start codon" Canine pro-endostatin coding sequence Location/Qualifiers 1. .693 ВР. 8 24-AUG-2001; 2001EP-00307224. 25-AUG-2000; 2000US-0227924P. AAL46062 standard; cDNA; 829 19-JUL-2002 (first entry) gynaecological; gene; ss (PFIZ) PFIZER PROD INC. Tong X; Canis familiaris. Sheppard MG, EP1191036-A2 27-MAR-2002. AAL46062; AAL46062 721 GAGGGGGCGCCCGCAGGAGCATCCGCCGCCCCGGGGGGCCTGGCCGGGACGCTTGCCTG 780

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The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, osler-webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, necessal anteriorence maniformations, ischaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine pro-endostatin coding sequence
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                                                       Claim 2; Fig 2; 56pp; English
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Matches 829; Conservative
                    endostatin protein.
related disorder,
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Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopath; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; angiofibroma; wound granulation; coronary collateral; cerebral collateral; arteriovenous malformation; coronary collateral; schemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiathritic; antipsoriatic; antidiabetic; ophthalmological; gynaecological; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, rounal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, mycardial angiogenesis, plaque neovascularisation, telangiactessia, haemophiliac joints, angiofibroma, arteriovenous malformations, colnaterals, cerebral collaterals, arteriovenous malformations, is chemenic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An isolated nucleic acid molecule for the treatment of angiogenesis-
related disorder, such as cancers or diabetic retinopathy, encodes an
  781 CACCGTCACGTTTAATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 829
                          781 CACCGTCACGTTTAATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 829
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1. .552
/*tag= a
/product= "Endostatin"
/product= "Does not include stop codon"
/partial
         100.0%; Pred. No. 7.8e-82; ive 0; Mismatches 0;
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Matches 555; Conservative
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139 CACACCCACCAGGACTTCCAGCTGGTGCTGCACCTGGTGGCCCTGAACAGGCCCGCAGCCG 198

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GTGCGCCGCGCCGCACCGCACCGCGCGCCCCGTCAACCTCAGGGACGAGGTGCTCTTC 378

GTGCGCCGGCCGACCGCACCGCACCGGGGTCGTCGTCAAACCTCAGGGACGAGGTGCTCTTC

181

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439 301 499

498

TTCTCTTTCGACGGCAGAGATGTCCTGCAGCACCCCGCCTGGCCCCGGAAGAGGCGTGTGG 360

CACGGCTCCGACCCCAGCGGGCGCCCTGACCGACACACTGCGAGACGTGGCGGACG 558

241 cccadcrogcadedcrrafrcrcedecrceaedeccadcreaacceegedeceedafe 300

CCCAGCTGGGAGGCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATC

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25-AUC-1999, 99WO-USO19329.

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Z5-AUC-1999, 99WO-USO19329.

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LEXI.) LEXINGEN PHARM CORP.

LO K, Li Y, Gillies SD;

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WPI; 2000-2376[6]20.

DR P-PSDB; AAY70265.

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WPF; 2000-2376[6]20.

RPSDB; AAY70265.

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WPF; 2000-2376[6]20.

DR P-PSDB; AAY70265.

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g	361 CACGGCTCCGACCCCAGCGGGCGCCCTGACCGACAGCTACTGCGAGACGTGGCGGACG 420	
à	559 GAGGCCCCGGCGCCACCGGGCAGGCGTCGTCGCTGCTGGGGGGGCAGGCTGCTGGAGCAG 618	
q	421 GAGGCCCCGGCCGCCACCGGCCAGCGTCGTCGTCGTGGTGGTGGTGTTTTTTTT	
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3 (
g 8	679 TCCTTCTCCAAG 690 541 TCCTTCTCCAAG 552	
RESI		
e ă	ABQ549S5 standard; cDNA; 4875 BP.	
S X	ABQ54955;	
E X	22-AUG-2002 (first entry)	
(B)	Human ovarian antigen HEEBK29 cDNA, SEQ ID NO:835.	
€	Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;	
2 2 3	ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; prepancy disorder; anovulation; polycystic ovary syndrome; pones;	
<u> </u>	inflammatory condition; immune disorder; blood disorder; intection;	
<u> </u>	cardiovascular disorder; respiratory disorder; neurological disorder; qastrointestinal disorder: urinary system disorder: daya sareenian.	
X §	gene therapy; chromosome mapping; forensic analysis;	
Z Z Z	antinflammatory; gynaecological; reproductive; chromosome 21q22.3; gene; ss.	
\$ 8	Homo sapiens.	
X X	WO200200677-A1.	
ž £	03 - JAN - 2002,	
X	S TO STITE ON TO CO.	
X	; TOOZ - NOO-	
K X	07-JUN-2000; 2000US-0209467P.	
P.A.	(HUMA-) HUMAN GENOME SCI INC.	
id:	Birse CE, Rosen CA;	
388	WPI; 2002-147878/19. P-PSDB; ABP41878.	
ž E	ed nucleic acid molecules encoding novel	
PT PT	evention, treatment and d lisorders, cardiovascular	
XX	Claim 1: SEO ID NO 835. 2922mm. English	
X	ייין און און אין אין אין אין אין אין אין אין אין אי	
ပ္ပပ္ပ	The invention relates to 2175 novel human ovarian antigens (ABP41054- ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also	
មួម	encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention The invention additionally related to	
88	antigen	
ខ្លួ	an	
86	ast-relate	
ខ្លួ	such conditions include ovari tumours of ovarian or breast	
ဥ္ပပ္မ	disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine	

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disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome). inflammatory conditions (e.g., mastitis, cophoritis and vaginitis), immune disorders (e.g., congenital and acquired communities, autolimmune cophoritis, systemic lupus erythematosus), cardiovaecular disorders, blood related disorders (e.g., anaemia), cardiovaecular disorders, respiratory disorders, neurological disorders gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polymucleotides may also be used in screening for compounds which modulate ovarian autigen expression or activity. The polymucleotides may further be used for gene therapy, chromosome mapping, in the contribution of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease disgnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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Pred. No. 1.8e-73;
0; Mismatches 153; Indels 39;
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P-PSDB; AAY08694.
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1966 GGCAGGCTCCTGGGCCAGAGTGCCGCGAGCTGCCATCACGCCTACATCGTGCTCTGCATT 2025 1906 idrakakardidacakadakadeneeneeneekaadeekadadeeneekadeeneeneeka 720 2026 GAGAACAGCTTCATGACTGCCTCCAAGTAGCCACCGCCTGGATGCAGATGGCCGGAGAGG 2085 2086 ACCGGCGGGCTCGGAGGAAGCCCCCACCGTGGGCAGGAGGAGCAGCCGGCCAGCCCTGGCCC 2145 2146 CAGGACCTGGCTGCCATACTTTCCTGTATAGTTCACGTTTCATGTAATCCTCAAGAAATA 2205 813 This invention describes a novel method for identifying mimetics of mammalian endostatin. The method comprises identifying a compound having atomic coordinates with non-trivial similarity to selected coordinates of atoms of a mammalian endostatin involves (a) providing a library of atomic coordinates of compounds in a library of candidate compounds, (b) Alphal(XVIII) collagen; mimetic; endostatin; atomic coordinate; library; anti-anglogenic; heparin binding domain; receptor binding domain; mimic; alpha-helix A domain; carbohydrate recognition domain; CRD domain; treatment; angiogenesis; tumour; human; se. 601 GGCAGGCTGCTGGAGCAGGAGGCGGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATC 661 GAGAACAGCGTCATGACCTCCTTCTCCCAAGTAGGGCCGCGGGGGCCCAGGGACAGGGGGG 757 -- GGGCCTGGCCGGGACGCTTGCCTGCACGG-TCACGTTTAATGTAATCCTCAAGAAATA /product= "alpha1(XVIII) collagen" /note= "Partial sequence, no start codon given" Olsen BR, Hohenester E, Timpl R, Sasaki T; Identifying mimetics of mammalian endostatin. Location/Qualifiers 1. .2055 Disclosure; Fig 5A-C; 75pp; English Human alphal (XVIII) collagen cDNA. AAX78379 standard; cDNA; 3394 BP. 2206 AAAGGAAGCCAAAGAG 2221 814 AAAGGAAGCCAAAGAG 829 98WO-US026783. 97US-0069727P 25-AUG-1999 (first entry) /*tag= a (HARD) HARVARD COLLEGE WPI; 1999-395243/33. P-PSDB; AAY25113.

comparing the library of atomic coordinates to the selected coordinates of a mammalian endostatin and (c) selecting from the library at least one candidate compound on the basis of selecting criteria which include similarities between the atomic coordinates of the selected candidate compound and the atomic coordinates of the mammalian endostatin. The invention also describes the use of an anti-anglogenic fragment of endostatin comprising a domain selected from a heparin binding domain, a receptor binding domain, and exposed on alpha helix A domain, and a reabolydrate recognition domain (CRD) domain. The methods can be used for designing and selecting endostatin minics. The compounds identified can be used for treating undesired anglogenesis, e.g. tumours. This sequence encodes human alphal (XVIII) collagen which is used in the description of

Sequence 3394 BP; 668 A; 1130 C; 1080 G; 516 T; 0 U; 0 Other;

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CCCGGGGCCCCGCACCACGGCTCCTACGTGCACTTCCAGCCGGGTCGCCCCACTGGTGGG cccredececeangardarcarccredeceaecececeaecredecredececaaecerad CAGCAGGCGCGGGGGGCTGGCGGGGCACCTTCCGCGCGCTTCCTGTCCTCCCCGCG Tereadacerdecedadedecreerredecededecededecercerederecedede Accederacercedadececedadecedadecadecadecadecadececercedece --GGGCCTGGCCGGGACGCTTGCCTGCACCG-TCACGTTTAATGTAATCCTCAAGAAATA CCCTGGCGGGCAGATGACATCCTGGCCGGCCCCCGGCCTGCTGGACCCCCAAGCCTAAC CTGAACAGCCCGCAGCCGGCCATGCGAGGCATCCGGGGAGCGGACTTCCAGTGCTTC CAGCAGGCGCGCGCGGGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTG AGGGACGAGGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTCGGGGCTCCGAGGGCCCAGCTG 1726 AAGGACGAGCTGCTGTTTCCCAGCTGGAGGCTCTGTTCTCAGGCTCTGAGGGTCGGCTG AAGCCCGGGGCCCCCATCTTCTTTTCGACGGCAGATGTCCTGCAGCACCCCGGCTGG CCCCGGAAGAGCGTGTGGCACGGCTCCGACCCCAGCGGCGCCCTGACCGACAGCTAC cocagaagagogreregeargecrosgacoccaacgeogecagocrosaccagagorac TOCGAGACGTGGCGGAGGCCCCCGGCGCCACGGGCAGGCGTCGTCGCTGCTGGCG GAGAACAGCGTCATGACCTCCTTCTCCAAGTAGGGCCGCGCGCCCCCACGGACAGGCGGGG <u> gadaacaderricardacrocerecanos adenados de astacadardos con da astacadadados de astacadadados de astacadadados de astacados de astacad</u> 121 CCCGTCCACACCCACACCCACACCCACACCACAGCTGCTGCTGCTGCTGGTGGCC CAGGACCICIACAGCAICGIGCGCCGCCGACCGCACCGGGGTGCCCGTCGTCAACCIC 39; Gaps Query Match 59.9%; Score 496.8; DB 2; Length 3394; Best Local Similarity 77.1%; Pred. No. 2.16-72; Matches 660; Conservative 0; Mismatches 157; Indels 39; 1906 181 1606 1846 541 1966 721 Н 1378 61 241 301 361 421 481 601 661 757 g g 쉱 8 8 g à g g δ õ g à a ઠે В \rightarrow \text{q} 8 ď જ ò ò ò ò

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ABK09977 standard; DNA; 900 BP
                   21-MAY-2002 (first entry)
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RESULT 9
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Synthetic plasmid pEnd-HR#1 FPD fusion DNA sequence.

Mouse; Ig signal peptide; mIgSP; functional protein domain; FPD; primary translational product; PTP; DNA construct; regulatory DNA; DNA targeting segment; regulatory factor; single regulatory unit; monoclonal antibody; recombination-derived alteration; blood product; human; COL18A1; gene; mutant; fusion protein; ds.

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Mus sp.
Homo sapiens.
Synthetic.
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The present invention relates to a new method of producing a protein, such as functional protein domain, that is either C or N-terminus of the primary translational product (PTP) of a gene, where the protein has biological activity which is distinct from PTP. The method of the invention involves growing a host cell transfected with a DNA construct comprising a regulatory DNA and a DNA targeting segment. This method is useful for producing a functional protein domain of proteins such as regulatory blood products and monoclonal antibodies. The method described in the invention allows controlled and precise modification of the host cell genome in order to produce functional protein domain (FPD) of the host cell genome is equence to be integrated in the host cell genome or coling sequence, the original coding sequence present in the host cell genome translet is used. Use of the host cell senon encoding FPD also provides the advantages of both eliminating any use of the same post-transcriptional (e.g., splicing) and/or post-translational (e.g. glycosylation, phosphorylation) processes that are
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                                                                                   note= "Mouse Ig signal peptide (mIgSP) exon"
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note= "Human COL18Al protein exons 38-41"
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/note= "Mouse Ig signal peptide (mIgSP)"
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/product= "pEnd-HR#1 FPD fusion protein"
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actually applied in vivo for the maturation of FPD. The use of a single regulatory unit eliminates the necessity of manipulating the complementary DNA coding for the PTP to isolate the segment coding for the PPD; and adapt it to the expression vector. The present nucleic acid sequence encodes the plasmid pEnd-HR#1 FPD fusion protein of the invention. The FPD fusion protein contains the mouse Ig signal peptide (mIgSP) sequence fused to exons 38-41 of the human COLIBAl sequence
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Human collagen XVIII coding

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising a DNA encoding an anti-angiogenic protein, which shows therapeutic effects on rheumatoid arthritis. The composition is useful for treating rheumatoid arthritis and the gene therapy is effective, lasting for 14 days. The present sequence is the coding sequence for human collagen XVII. Endostatin, which consists of the C-terminal 183 residues of collagen XVIII, was used as an anti-angiogenic protein
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Human, antirheumatic, antiarthritic, gene therapy; anti-angiogenic; rheumatoid arthritis; collagen; endostatin; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition for gene therapy against rheumatoid arthritis, comprising a DNA encoding anti-angiogenic protein or its parts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to a composition for gene therapy
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                                                                                                                                                                          "Human collagen XVIII'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 60-70; 84pp; English.
                                                                                                       Location/Qualifiers
1. .4551
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cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polymuclectides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the timour cells, in vaccines and for gene therapy. Note: The sequence date for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                               59.5%; Score 493.2; DB 6; Length 4551; 83.9%; Pred. No. 7.8e-72; Live 0; Mismatches 98; Indels 12;
                                                                                                                                                                                                      Sequence 4551 BP; 780 A; 1597 C; 1522 G; 652 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a fusion protein of vaa and endostatin. The specification describes a method for the production of soluble, recombinant human endostatin in Streptomyces. Leader sequences of streptomyces sp. strain CS SnpA and S. venezuelae alpha-amylase proteins are linked to the N-terminal of endostatin. This ensures that endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. The method is used for preparing soluble recombinant human, murine or primate endostatin, which is useful in the treatment of cancer, inhibition of tumour growth, inhibition of angiogenesis, isolation of receptors for endostatin and for identification of anti-angiogenic compounds in assays. The endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. Streptomycetes are amenable for cultivation in large fermentations allowing for large quantities of soluble endostatin to be produced
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Streptomycete host with expression vector comprising nucleotide sequence
encoding endostatin operably linked to linker and leader peptide.
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Streptomyces sp. strain C5; SnpA; S. venezuelae; alpha-amylase; endostatin; cancer; tumour growth; angiogenesis; ss.
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51.3%; Score 425.6; DB 3; Length 968;
Best Local Similarity 83.0%; Pred. No. 9.1e-61;
Matches 485; Conservative 0; Mismatches 99; Indels 0
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                                                                                                                                                Location/Qualifiers
220. .234
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/*tag= b
318. .968
/*tag= c
318. .401
/*tag= d
/note= "vaa signal sequenyce"
/*tag= d
/note= "edostatin"
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P-PSDB; AAB30495.
                                                                                           Streptomyces sp.
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                                                                                                                                                       Key
misc_binding
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558 340 618 400 678 460 738 520 798 580 858 640 918 Human, endostatin; IgG1Fc; tumour; vascular endothelial proliferation; vascular endothelial cytopoiesis inhibiting factor; inhibitor; fusion construct; ds. sel aggogrogrogragorgagogagorgacracragagogagogagogagogagoracogocaago CGGGCTCCGAGGCCAGCTGAAGCCCGGGGCCCGCATCTTCTTTTCGACGGCAGAGATG 439 CGGTGCTCCACCTGGTTGCGCTCAACAGCCCCTGTCAGGCGGCATGCGGGGCATCCGCG cerrereregeacracaecrecreratacaecaregeacecececeseace acordecedrogreaacercaaceaceacercerceccaacercearrier 619 ccórdeceardereaacheaadadadadereererreceaderadadadadeerererrer TOCTGCAGCACCCCCCCCCCCCCCCGAAGACGTGTGGCACGGCTCCGACCCCAGCGGGC googcoranaccadoracraccadados de costos dos dos costos dos costos dos costos dos costos de costos GAGCGGACTICCAGIGCTICCAGCAGGCGCGCGCCGCGGGGCTGGCCGGCACCTICCGGG /*tag= a /product= "endostatin/IgG1Fc construct" /transl except= (pos58. .60,aa:Ala) /transl_except= (pos:811. .816,aa:GGGGSGG) CCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACCTCCTTC 684 CCTACATGGTGCTCTGCATTGAGAACAGCTTCATGACTGCTCC 962 DNA encoding human Endostatin/IgG1Fc fusion construct. 8 (LIAO-) LIAONING WEIXING BIOLOGICAL PROD INST Location/Qualifiers 1. .1527 ABQ76740 standard; DNA; 1564 BP 30-NOV-2000; 2000CN-00123347. 30-NOV-2000; 2000CN-00123347. 03-MAR-2003 (first entry) Li Z, Liu Q; WPI; 2002-751441/82. P-PSDB; ABG73586. Homo sapiens. Synthetic. 19-JUN-2002 ABQ76740; 341 619 461 641 221 66 281 559 401 739 521 799 919 Chen L, 8

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This invention describes a novel method for the preparation of recombinant human vascular endothelial cytopoiesis inhibiting factor with human igGIFC fragment molecular structure and its product application. The novel factor is derived from endostatin (using PCR to screen a human foetal kidney cell cDNA library) and human IgGIFC. The product of the invention can specifically inhibit tumour vascular endothelial prolification and can be used for curing several tumour types. This sequence encodes a fusion construct composed of human endostatin and human IgGIFC, described in the disclosure of the invention
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                                   Preparation of recombinant human vascular endothelial cytopoiesis suppressor factor with human LgG1Fc fragment molecular structure and application of its product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1564 BP; 346 A; 491 C; 436 G; 291 T; 0 U; 0 Other;
                                                                                                                                                                                 Disclosure; Page 7-8 (Disclosure); 12pp; Chinese.
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Matches 528; Conservative
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A cDNA clone (AAT84485) codes for a mouse novel type alpha-1 (XVIII) collagen (AAW26328) that is expressed in multiple organs, especially the liver, lung and kidney. It was isolated by screening murine 15.5- and 17.5-day embryo libraries with probes based on murine type XII collagen and on human alpha-1 collagen cDNA. Isolated nucleic acids can be used to express recombinant alpha-1 collagen in transformed host cells. Claimed nucleic acid (see AAT84484) coding for human alpha-1 collagen (AAW26327) can be used to treat patients suffering from diseases associated with degradation of cartilage, and for supplementing collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3184 CCCTGGCGAGCAGATGACATCCTGGCCAACCCACCGCGCCTGCCAGACCGCCAGCCTTAC 3243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3300 -----CTCTCACTTGCTCATACTCATCAGGACTTTCAGCCAGTGCTCCACCTGGTG 3351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3352 GCACTGAACACCCCCCTGTCTGGAGGCATGCGTGGTATCCGTGGAGCAGATTTCCAGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding human alpha-1 collagen - for production of recombinant alpha-1 collagen, for use in the treatment of cartilage
                                                                                                                                                                   Alpha-1 collagen; type XVIII collagen; cartilage degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4031 BP; 873 A; 1172 C; 1266 G; 720 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4031;
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51.0%; Score 423; DB 2; Length 403
Best Local Similarity 76.9%; Pred. No. 2.2e-60;
Matches 548; Conservative 0; Mismatches 150; Indels
                                                                                                                                                                                                                                            Location/Qualifiers
1. .3867
/*tag= a
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                    AAT84485 standard; cDNA; 4031 BP.
                                                                                                                                                                                                                                                                                                                                                                                              93US-00159784.
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                                                                                                                                 Mouse alpha-1 collagen cDNA.
                                                                                             (first entry)
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                                                                                                                                                                                                          Mus musculus.
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                        3472 CTGCAGGATCTCTATAGCATCGTGCGCGTGCTGACCGGGGGGTCTGTGCCCATCGTCAAC 3531
                                                                                                                                              TACTGTGAGACATGGCGAACTGAAACTACTGGGGCTACAGGTCAGGCCTCCTCCTCCTGCTG 3771
                                                                                                                                                                                                                                                                                                                             CCGAGGCCAG 417
                                                                                                                   CTGAAGCCCCGGCCCCCCATCTTCTTTCGACGCCAGAGATGTCCTGCAGCACCCCGCC 477
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CTGCAGGACCTCTACAGCATCGTGCGCGCGCCGACCGCACCGGGGTGCCCGTCGAC 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiogenesis inhibitor, KED, kringle protein, angiogenesis, tPA, tissue plasminogen activator; tumour; atherosclerosis; arthritis; retinopathy; bronchial vascular congestion; inflammatory bowel disease; adult respiratory distress syndrome; Castleman's disease; psoriasis; hepatitis; aneurysm; renal disease; haemangioma; ss.
                                                                                                                                                                                                                                      TACTGCGAGACGTGGCGGACGGAGGCCCCGGGCCACCGGGCAGGCGTCGTCGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                        3832 ATTGAGAATAGCTTCATGACCTCTTTCTCCAAATAGGCCTCTGCCAGCTAGGG 3884
                                                                                                                                                                                                                                                                                                                                                          Use of kringle protein and kringle derived from plasminogen and composition comprising kringle proteins for treating tumor and atherosclerosis, arthritis and retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding a human angiogenesis inhibitor designated KED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag≈ a
/product= "angiogenesis inhibitor KED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chopp M, Wang L, Mikkelsen T;
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1. .816
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99US-0166176P
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The present sequence encodes a human polypeptide which is a potent anglogenessis inhibitor, designated KED. The KED polypeptide, Kringle proteins, or a kringle derived from human tissue plasminogen activator (tPA) protein are used to inhibit anglogenesis. Kringle protein, KED or the pare useful for treating tumours, as well as atherosclerosis, arthritis, retinopathy and other similar diseases. KED is also useful for the treatment of diseases such as bronchial vascular congestion, the treatment of disease, adult respiratory distress syndrome, castleman's disease, psoriasis, hepatitis, aneurysm, renal disease and haemangioma
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Sequence 31, Appli
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Sequence 3, Appli
Sequence 6, Appli
Sequence 6824, Ap
Sequence 1793, Ap
Sequence 1793, Ap
                                                                      March 29, 2004, 10:57:20 ; Search time 83.8584 Seconds (without alignments) 5486.086 Million cell updates/sec
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                                                                                                                       US-09-938-391-1
829
1 ccctggcgggcagatgacat......aataaaaggaagccaaagag 829
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 US-08-159-784-1
4 US-08-231-77D-9
4 US-09-315-689-4
3 US-09-315-689-6
4 US-09-315-689-6
4 US-09-561-500-12
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1 US-09-231-077D-7
1 US-09-231-077D-8
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                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                             682709 seqs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
Sequence:
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Sequence Seq		th 3394; ts 39; saccccac	BAGCCCCAC
u a v	THEREOF	1; Length 7; Indels GCCTGCTGGA	GGCTGCCO
991A-1206 991A-1194 991A-11861 991A-2173 991A-2173 508-3 100-7 742-7 742-7 742-7 742-7 609-3 100-7 609-1 609-1 609-1	USES .	496.8; DB No. 2e-86; smatches 15 3ccGccccccc	GCCCCCTG
US-09-252-991A-11 US-09-252-991A-11 US-09-252-991A-11 US-09-252-991A-21 US-09-252-991A-21 US-09-2016-537-1 US-09-091-609-3 US-08-265-310-7 US-08-265-310-7 US-08-265-310-7 US-08-265-310-7 US-08-265-310-7 US-08-265-310-7 US-08-265-310-7 US-08-265-310-7 US-08-265-310-7 US-08-265-310-7 US-08-265-310-7 US-08-265-310-7 US-08-265-310-7 US-08-269-310-7 US-08-269-310-7 US-08-269-310-7 US-08-269-310-7 US-08-269-310-7 US-08-269-310-7 US-08-269-310-7 US-08-269-310-7 US-08-268-310-7 US-08-268-310-7 US-08-268-310-7	ALIGEN 1.44 1.44 1.59,78 1.59,78	S9.9%; Score 496.8; DB 1; Length ilarity 77.1%; Pred. No. 2e-86; Conservative 0; Mismatches 157; Indels credecaccocccececcreara.	CCTGGGGGGGAGATGACATCCTGGCCAGCCCCCTGGGCTGCCCGAGCCCAAGCC
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1438 CCCGGAGGCCCGCACCACACGCTCCTACGTGCACTGCGCCCGGCACGACCCACGAG---- 1493
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121 CCCGTCCACACCCACACCCACACCCAGACTTCCAGCTGGTGCTGCTGGTGGCC 180
                                                                                                                                                                                                                                            241 CAGCAGGCGCGCGCGCGGGGGCTGGCCGGCACCTTCCGGGGCCTTCCTGTCGTCGCGGCTG 300
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RESULT 2
US-08-159-784-1
Sequence 1, Application US/08159784
Fatent No. 5643783
GENERAL INFORMATION:
APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STRET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

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3184 CCCTGGCGAGCAGATGACATCCTGGCCAACCCACCGCGCCTGCCAGACCGCCAGCCTTAC 3243
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Best Local Similarity 76.9%; Pred. No. 2.3e-72;
Matches 548; Conservative 0; Mismatches 150; Indels 15; Gaps
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordferfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
                                                                                                                                                                                                                                                                                                                                                      NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 0024!
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
                                                                                                                                                                                     December 1, 1993
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4031
                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                              FILING DATE: December CLASSIPTCATION: 530 PRIOR APPLICATION DATA: APPLICATION WINBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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US-08-159-784-1
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3772 TCAGGCAGGCTCCTGGAACAGAAGCTGCGAGACAGCACAACAGCTACATCGTCTGTGC 3831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498
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                                                                                                3832 ATTGAGAATAGCTTCATGACCTCTTTCTCCAAATAGGCCTCTGCCAGCTAGGG 3884
                                                           50.5%; Score 418.4; DB 4; Length 563; 84.5%; Pred. No. 1.5e-71; Live 0; Mismatches 86; Indels 0
                                                                                                                                                                                     Sequence 9, Application US/09231077D

PREENT NO. 6653098

GENERAL INFORMATION:
APPLICANT: Harding, E.I.
APPLICANT: Violand, B.N.
TITLE OF INVENTION: Method of producing mouse and human
TITLE OF INVENTION: Method of producing mouse and human
TITLE OF INVENTION: endostatin
FILE REFERENCE: S03071-00-US
CURRENT APPLICATION NUMBER: US/09/231,077D

PRIOR APPLICATION NUMBER: 60/075,587

PRIOR APPLICATION NUMBER: 60/075,587

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FASISEQ for Windows Version 4.0

SEQUENCE: S03071-00-US

SEQUENCE: S03071-00-US

SOFTWARE: FASISEQ for Windows Version 4.0
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Matches 470; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: human
                                                                                                                                                     RESULT 3
US-09-231-077D-9
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US-09-315-689-4

US-09-315-689-4

Sequence 4, Application US/09315689

Patent No. 6346510

GENERAL INFORMATION:

APPLICANT: FOlkman, Judah

APPLICANT: PARTICATION UNMER: US/09/315,689

CURRENT APPLICATION UNMER: 1999-05-20

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 4

LENGTH: 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens US-09-315-689-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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; TYPE: DNA ; ORGANISM: Homo sapiens US-09-315-689-6

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181 GTGCGCCGTGCCGACCGCGCAGCCGTCCTCCAACTCAAGGACGAGCTGCTGTT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CACAGCCACCTOCCACTTCCAGCCGGTGCTCCACCTGGTTGCGCTCAACAGCCCCCTGTCA 60
; TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and
TITLE OF INVENTION: Proteins and Methods of Use
FILE REPERBUSE: 05213 0370
CURRENT APPLICATION NUMBER: US/09/206,059
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 552
TYPE: DNA
CREANTSH: Homo sapiens
US-09-206-059-30
                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                Query Match 50.4%; Score 418; DB 3; Length 552; Best Local Similarity 85.3%; Pred. No. 1.8e-71; Matches 466; Conservative 0; Mismatches 80; Indels
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Sequence 6, Application US/09315689
Fatent No. 6346510
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REPREMENCE: 08213-0229
CURRENT APPLICATION NUMBER: US/09/315,689
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
LENGTH: 534
RESULT 6
US-09-315-689-6
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480
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                                                                                                                                                                                                                                                                                                                             121 ACCTICGGGGCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATCGTGCGCCGTGCC 180
                                                                                                                                                                                         Sequence 12, Application US/09561500
| Sequence 12, Application US/09561500
| Patent No. 634219
| GENERAL INPORMATION:
| APPLICANT: Philip E Thorpe
| APPLICANT: Rolf A. Brekken
| TITLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
| FILE REPREBNCE: 4001.005500
| CURRENT APPLICATION NUMBER: 4001.005500
| CURRENT FILING DATE: 2000-04-28
| PRIOR FILING DATE: 1999-04-28
| NUMBER OF SEQ ID NOS: 444
| SOSTWARE: PATENTIN VET. 2.0
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                                                .,
Query Match
49.6%; Score 410.8; DB 4; Length 534;
Best Local Similarity 85.6%; Pred. No. 4.3e-70;
Matches 457; Conservative 0; Mismatches 77; Indels 0
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Pred. No. 1.3e-63;
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; LOCATION: (1)..(573)
US-09-561-500-12
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Best Local Similarity
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LENGTH: 573
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Qy 126 CCACACCCACACCCACAGACTTCCAGCTGCTGCTGCTGCTGCTGCTGAA 185	Db 9 CCATCACCATCACCATCATACATCACCAGGGCCCAGGGCGCGGGGGGCGGGGGGGG	Db 69 CACCCCCTGTCTGGAGGCATGCGTGGAATCCGTGGAGATTTCCAGTGCTTCCAGGA 128 Oy 246 GGCGGGGGGGGGGGGGCGGCCGACCTTCCGGGGCCTGCTGGCGGA 305	Db 129 AGCCCGAGCCGTGGGGGCGTGTCGGGCTTCCGGGCTTTCCTGTCCTCTAGGCTGCAGGA 188 Qy 306 CTCTACAGCATCGGGGCGGGCCGACCGCACCGCACGGGGTCGTCGTCGTCAGGGA 365	Db 189 TCTCTATAGCATCGTGCCGTGCTGACCGGGGGGTCTGTGCCATCATCAACCTGAAGGA 248 Oy 366 CGAGGTGTTTCCCCAGCTGGAGGCCTTATTCTCGGGCTCGAGGGCTGAAGCC 425	Db 249 CAAGGTGTAICTCCCAGTTGCACTCCTGTTTTCTGGCTCCCAGGGTCAACTGCAACC 308 Oy 426 CGGGGCCGGCATCTTTTCGAGGAGAGAAGATCTCCTGCAGGACCCCGGCTGGCCCG 485	Db 309 cddddccddchfrffffffalddddddddddddddddddddchdddddddddddddddd	DD 369 GAAGAGCGTATGGGACCCCCAGGGGGGGGGGGGGGGGGG	Db 429 dalahdeldaaltralaaatraltradagcralaadercradecrictradercraderages 488 Qy 606 getgetragagagagagagagagagagagagagagagagagagag	Db 489 GTTCTGGGAGCTGCGACTGCCACAACAGCTACGGAA 548 Qy 666 CAGCGTCGCTGCCTCTCCCAA 689	Db 549 TAGCTTCATGACCTCTTTCTCCAA 572	200	; Sequence 12, Application US/US561526; Patent No. 6416758; Patent No. 6416758; Patent No. 6416758; Patent No. 6416758; Patent No. 6416778; Patent Representation: Amilia Dr. Thure of invention: Amilia Dr. Conjugate Kits for Selectively inhibiting vege; Patent Application Nuwber: US/09/561,526; CURRENT PILING DATE: 2000-04-28; PRIOR FILING DATE: 1999-04-28; PRIOR FILING DATE: 1999-04-28	; NUMBER OF SEQ ID NOS: 44 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 12 ; ISNGTH: 573 ; TYPE: DNA) ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: DESCRIPTION OF Artificial Sequence: SYNTHETIC ; OTHER INFORMATION: OLIGONUCLEOTIDE ; NAME/KEY: CDS ; LOCATION: (1)(573) US-09-561-526-12	Query Match 45.5%; Score 376.8; DB 4; Length 573; Best Local Similarity 79.3%; Pred. No. 1.3e-63; Matches 447; Conservative 0; Mismatches 117; Indels 0; Gaps 0;	cacccacacc
Matches 447; Conservative 0; Mismatches 117; Indels 0; Gaps 0;	OY 126 CCACACCCACCCACCCACCAGACTICCAGCIGGTGCTGCACCTGGTCCTGGCCTGAA 185	QY 186 CAGCCGCAGCGGCGATGCGAGGCATCCGGGAGCGGACTTCCAGTGCTTCCAGCA 245	OY 246 GGGGGGGGGGGGGGGGGGGCACCTTCCGGGCCTTCCTGTCGTCGGGGCTGCAGA 305	Qy 306 CCTCTACAGCATCGTGCGCCGCGCCGCACCGCGGGGTGCCCGTCGTCACCTCAGGGA 365 Db 189 TCTCTATAGCATCGTGCGCGCGTGCTGACCGGGGGTCTGTGCCCATCGTCAACCTGAAGGA 248	Qy 366 CGAGGIGCTCTTCCCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCC 425	Qy 426 CGGGGCCCGCATCTTCTCTTTCGACGGCAGGATGTCCTGCAGCACCCCGCCTGGCCCG 485	Oy 486 GAAGAGGTGTGGCACGGCTCCGACCCCAGGGGGCGCCGCTGACCGACGGTACTGCGA 545	Qy 546 GACGTGGCGGACGGACGCCCCGGCGCCACGCAGGCGTCGTCGCTGCTGCGGGGAG 605	OY 606 GCTGCTGGAGCAGGAGGCGCGCGCGCCCTTCGTGGTGCTCTGCATCGAGAA 665	9 1	scricalgaccicilicicoaa sy	RESULT 8 19.09-561-108-12 Sequence 12, Application US/09561108 Sequence 12, Application US/09561108 Setent No. 6342221 GENERAL INFORMATION: APPLICANT: Philip E. Thorpe APPLICANT: Rolf A. Brekken TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF TITLE REPERENCE: 4001.002584 CURRENT APPLICATION UNDREE: US/09/561,108	CORRENT FILLING DATE: 2000-04-28 PRIOR APPLICATION NUMBER: 60/131,432 PRIOR FILING DATE: 1999-04-28 NUMBER OF SEQ ID NOS: 44 SOUTHWARE: Patentin Ver. 2.0 SEQ ID NO 12	IDENGTH: 573 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: CTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC OTHER INFORMATION: OLIGONUCLEOTIDE NAME (NEW CREENT)	97. 0 37. 0 . B	

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9 CCATCACCATCACCATACTCAGGACTTTCAGCCAGTGCTCCACCTGGTGGCACTGAA 68
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APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002582
CURRENT APPLICATION NUMBER: US/09/561,499
CURRENT APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION TO BE : 60/131,432
PRIOR PILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENT IN Ver. 2.0
LENGTH: 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
SOGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: OLIGONUCLEOTIDE
TOTHER INFORMATION: OLIGONUCLEOTIDE
TOTHER INFORMATION: OLIGONUCLEOTIDE
TOTHER INFORMATION: OLIGONUCLEOTIDE
TOCATION: (1) .. (573)
US-09-561-499-12
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45.5%; Score 376.8; DB 4; Length 573;
Best Local Similarity 79.3%; Pred. No. 1.3e-63;
Matches 447; Conservative 0; Mismatches 117; Indels 0.
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/ Patent No. 6524583
/ GENERAL INFORMATION:
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Sequence 12, Application US/0999831

Sequence 12, Application US/0999831

Sequence 12, Application US/0999831

Sequence 12, Application US/0999831

Sequence 12, Application US/0998831

SERNEAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: Philip E. Thorpe

TITLE OF INVENTION: INHIBITING VEGF

TITLE OF INVENTION: INHIBITING VEGF

TITLE OF INVENTION UNMBER: US/09/998,831

CURRENT FILING DATE: 2001.11-30

PRIOR APPLICATION NUMBER: 09/561,108

PRIOR APPLICATION NUMBER: 09/561,108

PRIOR PELLING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 12

IENGTH: 573
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ORGANISM: Artificial Sequence
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247 ATCTCCCAGCTGCTCTCTTTTCTGGCTCCCAGGGTCAACTGCAACCGGGGGCCGG 306
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                                                                                                                                                          Score 376.6; DB 3;
Pred. No. 1.4e-63;
0; Mismatches 114;
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| Sequence 7, Application US/09231077D |
| Patent No. 6653098 |
| GENERAL INFORMATION: |
| APPLICANT: Harding, E.I. |
| APPLICANT: Violand, E.N. |
| TITLE OF INVENTION: Method of producing mouse and |
| TITLE OF INVENTION: Method of producing mouse and |
| PILE REFERENCE: S03071-00-US |
| CURRENT APPLICATION NUMBER: US/09/231,077D |
| PRIOR FILING DATE: 1999-01-14 |
| PRIOR FILING DATE: 1998-01-14 |
| PRIOR FILING DATE: 1998-02-23 |
| NUMBER OF SEQ ID NOS: 13 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| TYPE: DNA |
| TYPE: DNA |
| CRGANISM: human |
| CRG
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                                                                                                                                                          Query Match
Best Local Similarity 79.6%;
Matches 445; Conservative C
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
          ; TYPE: nuc); STRANDEDNES; ; TOPOLOGY: US-08-985-526-37
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APPLICANT: Uteza, Yves
APPLICANT: Uteza, Yves
APPLICANT: Wensache, Maurice
APPLICANT: Wensache, Maurice
APPLICANT: Bonnel, Sebastien
APPLICANT: Bonnel, Sebastien
APPLICANT: Bonnel, Sebastien
APPLICANT: Honiger, Jiri
CURRENT APPLICATION NUMBER: US/09/449,293
CURRENT APPLICATION NUMBER: US/09/449,293
CURRENT APPLICATION NUMBER: US/09/449,293
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 79.7%; Pred. No. 1.7e-63;
Matches 444; Conservative 0; Mismatches 113; Indels 0
al Similarity 79.4%; Pred. No. 1.5e-63;
446; Conservative 0; Mismatches 116; Indels
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CORGANISM: Rattus rattus
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APPLICANT: Abitbol, Warc

APPLICANT: Uteza, Yve6

APPLICANT: Weasache, Maurice

APPLICANT: Weasache, Maurice

APPLICANT: Wan Den Berghe, Loic

APPLICANT: Bonnel, Sebastian

APPLICANT: Bonnel, Sebastian

APPLICANT: Bonnel, Martin

APPLICANT: Honiger, Jiri

APPLICANT: Neuner-Jehle, Martin

FILE REFERENCE: 8006-2020ED1

CURRENT APPLICATION NUMBER: US 09/449,293

FRIOR FILING DATE: 1999-11-24

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LEMOTH: 558

TYPE: DNA

ORGANISM: Rattus rattus

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Best Local Similarity 79.7%; Pred. No. 1.7e-63;
Matches 444; Conservative 0; Mismatches 113;
Sequence 3, Application US/09775325 Patent No. 6500449 GENERAL INFORMATION:
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Search completed: March 29, 2004, 13:41:19 Job time : 89.8584 secs

Sequence 12, Appl Sequence 3, Appl Sequence 3, Appli Sequence 3, Appli Sequence 4, Appli Sequence 10, Appli Sequence 10, Appl Sequence 165, Appl Sequence 165, Appl Sequence 159, Appl Sequence 67, Appl Sequence 1103, Appl Sequence 1103, Appl Sequence 1203, Appl Sequence 1203, Appl Sequence 15103, Appl Sequence 193, Appl

537 14 US-10-131-241-59 540 14 US-00-998-831-12 553 14 US-00-998-831-12 558 19 US-00-998-831-12 558 9 US-00-775-174-3 624 13 US-10-1080-797-4 624 13 US-10-080-797-4 624 14 US-10-080-797-4 624 14 US-10-080-797-4 624 12 US-10-080-797-4 625 14 US-10-080-797-4 626 12 US-10-10-172-163 480 12 US-10-080-797-4 520 14 US-10-080-797-4 520 15 US-10-10-172-163 522 15 US-10-10-172-163 522 15 US-10-10-172-163 522 15 US-10-10-172-163 522 15 US-10-180-76-1 522 15 US-10-130-97-397-67 522 15 US-10-130-97-397-67 522 15 US-10-130-97-67 522 15 US-10-130-97-67 522 15 US-10-130-97-67 521 12 US-10-130-493-493-493-493-493-493-493-493-767-193 521 12 US-10-156-761

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Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-10-292-118-34

5 US-10-264-049-835

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4 US-10-322-418-3

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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

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RESULT 1
US-09-938-391-1
Sequence 1, Application US/09938391
Sequence 1, Application US/09938391
Sequence 1, Application No. US2030158099A1
GENERAL INFORMATION:
APPLICANT: Tong, et al.
TITLE OF INVENTION: DISORDERS INVOLVING ANGIOGENESIS
TITLE OF INVENTION: DISORDERS INVOLVING ANGIOGENESIS
TITLE OF INVENTION: US/09/938,391
CURRENT APPLICATION UNMER: 2001-08-24
SOFTWARE: PATENTIN Ver. 2.1
SOFTWARE: PATENTIN Ver. 2.1
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100.0%; Score 829; DB 10; Length
Best Local Similarity 100.0%; Pred. No. 1.7e-186;
Matches 829; Conservative 0; Mismatches 0; Indels
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; ORGANISM: CANINE PRO ENDOSTATIN NUCLEOTIDE SEQUENCE
US-09-938-391-1
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Best Local Similarity
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Publication No. US20030158099A1
Publication No. US20030158099A1
Publication No. US20030158099A1
Publication No. US20030158099A1
APPLICANT: Tong, et al.
APPLICANT: Tong, et al.
TILLE OF INVENTION: DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: PC10790A
CURRENT FILING DAID: 2010-08-24
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3
LENGTH: 555
                                                                                                                                                                                                                                                                                                                                                          481 CCCCGGAAGAGCGTGTGGCACGCTCCGACCCCAGGGGGCGCCGCCTGACCGACAGCTAC
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66.9%; Score 555; DB 10; Length 55
Best Local Similarity 100.0%; Pred. No. 8.3e-122;
Matches 555; Conservative 0; Mismatches 0; Indels
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       121 GGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATC 180
                                                                            GTGCGCCGCGCCGACCGCACCGGGGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTC 378
                                                                                                                   241 cccadcradaagaccrrarrcrcaagcrccaagacaagcraaagccaagacaagacaarc 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies;
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies;
FILE REFERENCE: PA13919
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 835, Application US/10264049 Publication No. US20040005579A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-264-049-835
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APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION NUMBER: US/10/292,418
CURRENT FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 60/097,883
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEC ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 552
121 GGGCTGGCCGCCACCTTCCGGGCCTGCGGGCTGCAGGACCTCTACAGCATC 180
                                             319 GIGGGCGGCGGACCGCACCGGGGTGCCCGTCGTCAACCTCAAGGACGAGGTGCTCTTC 378
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                                                                                      CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGGCCCGCATC
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Sequence 34, Application US/10292418
Publication No. US/20030139365A1
GENERAL INFORMATION:
APPLICANT: Lo, Kin. Ming
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OTHER INFORMATION: Endostatin
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ORGANISM: Canis familiaris
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Best Local S:
Matches 551
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2614 CAGCAGGCGCGGGGCCGTGGGGGGGGCGCCTTCCGGCGTCCTGCTCCTGCGCCTG 2673
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241 CAGCAGGCGCGCCGCGGGGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTG 300
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RESULT 6
US-09-880-107-2178

Sequence 2178, Application US/09880107

Patent No. US2002012981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Gene Logic, Uweeph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Enc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US 60/214,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2178

LENGTH: 3394

TYPE: DNA

TYPE: DNA

CORMANDEN: Homo sapiens
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2026 GAGAACAGCTTCATGACTGCCTCCAAGTAGCCACCGCCTGGATGCAGATGCCGGAGAGG 2085 'n 1438 CCCGGAGCCCGCACCACCACCTCCTACGTGCACTGCGGCCCCGGCACCCACAAG---- 1493 1546 CTCAACAGCCCCTGTCAGGCGGCATGCGGGCATCCGCGGGGCCGACTTCCAGTGCTTC 1605 1606 cadcadececedececerecececececececentececececerecerececececene 1726 AAGGACGAGCTGCTGTTTCCCAGCTGGAGGCTCTGTTCTCAGGCTCTGAGGGTCGCTG 1785 1378 CCCTGGCGGGCAGATGACATCCTGGCCAGCCCCCTGGGCTGCCCGAGCCCCAGCCCTAC 1437 420 1786 AAGCCCGGGGCACGCATCTTCTCCTTTGACGGCAAGGACGTCCTGAGGCACCCCCACCTGG 1845 1846 CCCCAGAAGAGAGGGTGTGGCTCGGACCCCAACGGGCGCAGGCTGACCGAGAGCTAC 1905 1906 TGTGAGACGTGGCGGACGGAGGCTCCCTCGGCCACGCCCAGGCCTCCTCGCTGCTGGGG 1965 1966 GGCAGGCTCCTGGGGCAGAGTGCCGCGAGCTGCCATCACGCCTACATCGTGCTCTGCATT 2025 1086 ACCGGCCGCTCGGAGGAAGCCCCCACCGTGGGCAGGAGCAGCCGGCCAGCCCCTGGCCC 2145 2146 caggaccregerecearacrirecreraragricacerireargrarecreaagaara 2205 121 CCCGTCCACACCCACACCCACACCCACCAGGACTTCCAGCTGGTGCTGCACCTGGTGGTGCC 190 241 CAGCAGGGGGGGGGGGGGGGGGGGGCAACCTTCCGGGGCCTTCCTGTCGTGGCGGCTG 300 CAGGACCTCTACAGCATCGTGCGCCGCCGGACCGCACCGGGGTGCCCGTCGACCTC 360 CCCGGGGCCCCGCACCACGGCTCCTACGTGCACTTCCAGCCGGCTCGCCCCACTGGTGGG 120 421 AAGCCCGGGGCCCGCATCTTTTTCGACGGCAGAGATGTCCTGCAGCACCCCGCGTGG 480 601 gecagecrecrigaagcagaagcceceaagcreccaccacccrrceregrecrecare 660 661 GAGAACAGCGTCATGACCTCCTTCTCCAAGTAGGGCCGCGGCGCCCACGGACAGGCGGGG 720 1 CCCTGGCGGGCAGATGACATCCTGGCCGGCCCCCCGCGCCTGCTGGACCCCCCAGCCCTAC 60 CTGAACAGCCCGCAGCCGGCCGCCATGCGAGGCATCCGGGGAGCGGACTTCCAGTGCTTC 361 AGGGACGAGGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTG CCCCGGAAGAGAGCGTGTGGCACGGCTCCGACCCCAGCGGGCGCCCCCGCCTGACCGACAGCTAC 541 TGCGAGACGTGGCGGACGGAGGCCCCGGCGGCCACCGGGCAGGCGTCGTCGCTGCTGGCG 757 --GGGCCTGGCCGGGACGCTTGCCTGCACGCTTTAATGTAATCCTCAAGAAATA Query Match 59.9%; Score 496.8; DB 9; Length 3394; Best Local Similarity 77.1%; Pred. No. 4.2e-108; Matches 660; Conservative 0; Mismatches 157; Indels 39; Gaps 2206 AAAGGAAGCCAAAGAG 2221 814 AAAGGAAGCCAAAGAG 829 181 481 301 윱 셤 ઠે ద à 셤 ઠે g ò 셤 ठे g g à a ઠે a g ò ò ò ò à

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RESULT 7

Sequence 144, Application US/10060036

Publication No. US20030073144A1

GENERAL INFORMATION:

APPLICANT: Benson, Darin R.

APPLICANT: Kalos, Michael D.

APPLICANT: Lodes, Michael J.
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L22548 US-09-880-107-2178

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Best Local Similarity 83.9%; Pred. No. 2.9e-107;
Matches 574; Conservative 0; Mismatches 98; Indels 12; Gaps
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210.121.56 US/10/060,036
CURRENT APPLICATION UNMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 144
LENGTH: 4551
TYPE: DNA
ORANISM: Homo sapiens
US-10-060-036-144
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TYPE: DNA
CORGANISM: Homo sapiens
US-10-042-347-4

| JERREAL INTOGRAPHICANT: O'Really, Michael S. |
| APPLICANT: O'Really, Michael S. |
| APPLICANT: O'Really, Michael S. |
| APPLICANT: O'Really, Michael S. |
| TITLE OF INVENTION: Nucleic Acid Molecules Encoding Endostatin Protein and Peptide F. |
| TITLE OF INVENTION: Thereof S. |
| TITLE OF INVENTION: UNMERR: US 09/154,307 |
| PRIOR PLICATION NUMBER: US 09/154,302 |
| PRIOR PLICATION NUMBER: US 09/154,302 |
| PRIOR PLICATION NUMBER: US 09/154,302 |
| PRIOR PLICATION NUMBER: US 00/005,835 |
| PRIOR PLICATION NUMBER: US 00/005,835 |
| PRIOR PLICATION NUMBER: US 00/005,835 |
| PRIOR PLICATION NUMBER: US 00/005,035 |
| PRIOR PLING DATE: 1996-09-17 |
| PRIOR PLING DATE: 1996-09-17 |
| PRIOR APPLICATION NUMBER: US 00/005,035 |
| PRIOR APPLICATION NUMBER: US 00/005,035 |
| PRIOR PLING DATE: 1996-09-17 |
| PRIOR APPLICATION NUMBER: US 00/005,035 |
| PRIOR APPL

GENERAL INFORMATION:

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                                                                   0; Gaps
Length 546;
                                                                   80; Indels
      Query Match 50.4%; Score 418; DB 14; Best Local Similarity 85.3%; Pred. No. 1.8e-89; Matches 466; Conservative 0; Mismatches 80;
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RESULT 8 US-10-042-347-4 ; Sequence 4, Application US/10042347 ; Publication No. US20030114370A1

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NAME/KEY: CDS

| LOCATION: (1)..(549)

| OTHER INFORMATION: endostatin

US-10-292-418-3
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Best Local Similarity
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CORGANISM: Homo sapiens
US-10-131-241-53
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gequence 30, Application US/09873676

patent No. USC02007728941

GENERAL INFORMATION:

APPLICANT: MacDonald, Nicholas J.

APPLICANT: Sim, Kim L.

ITILE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use

FILE REPERBNCE: 05213-0378 (43170-255333)

CURRENT APPLICATION NUMBER: US/09/873,676

CURRENT PLING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-06

PRIOR PLING APPLICATION NUMBER: US 60/289,387

PRIOR FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 123

SOFTWARE: Patentin version 3.1

SEG ID NO 30

LENGTH: 552
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Matches 466; Conservative
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CORGANISM: Homo sapiens
US-09-873-676-30
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RESULT 12 US-10-080-797-2 Sequence 2, Application US/10080797 Publication No. US20020183253A1

GENERAL INFORMATION

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                                                                                                                                                                          Length 551;
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                                                                                                                                                                          50.3%; Score 417; DB 13;
85.3%; Pred. No. 3.1e-89;
tive 0; Mismatches 80;
APPLICANT: Campochiaro, Peter A.
APPLICANT: Dixon, Katharine H.
APPLICANT: Dixon, Katharine H.
APPLICANT: Brazzell, Komulus K.
TITLE OF INVENTION: METHOD FOR TREATING OCULAR
TITLE OF INVENTION: NEOVASCULARIZATION
FILE REPERENCE: 4-31881A
CURRENT APPLICATION NUMBER: US/10/080, 797
CURRENT PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 551
                                                                                                                                                                            Query Match 50.3
Best Local Similarity 85.3
Matches 465; Conservative
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                                                                                                                                TYPE: DNA

CRGANISM: Human
US-10-080-797-2
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Li, Li
Ji, Weizhen
Padigaru, Muralidhara
Casman, Stacie
Voss, Edward
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; LOCATION: (1)..(552)
US-10-210-172-161
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CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1399-10-06
PRIOR PILING DATE: 1399-05-21
PRIOR PILING DATE: 1999-05-21
PRIOR PILING DATE: 1999-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PRECEIT Version 3.1
LENGTH: 632
                                                                                                                                                                                                                                                       Best Local Similarity 82.8
Matches 523; Conservative
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Best Local Similarity 84.6%; Pred. No. 5.8e-88;
Matches 462; Conservative 0; Mismatches 84; Indels 0;
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Sequence 161, Application US/10210172; Publication No. US20040043928A1; GENERAL INFORMATION: APPLICANT: Kekuda, Ramesh APPLICANT: Miller, Charles APPLICANT: Patturajan, Meera APPLICANT: Petturajan, APPLICANT: Peturajan,

RESULT 14 US-10-210-172-161

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                                                  CCCAGCTGGGAGGCCTTATTCTCGGGGCTCCGAGGCCCAGCTGAAGCCCGGGGCCCGCATC 438
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                         GTGCGCCGCCGACCGCACCGGGGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTC
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CORGANISM: Homo sapiens
US-10-042-347-6
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Gaps

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March 29, 2004, 11:07:01 , Search time 2546.3 Seconds (without alignments) 9722.244 Million cell updates/sec US-09-938-391-1 829 1 ccctggcgggcagatgacat......aataaaaggaagccaaagag 829 55026578 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 27513289 seqs, 14931090276 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 em gss pro: *
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em_estfun:* em_estom:* em_gss_hum:* EST:* Title: Perfect score: Scoring table: Searched: Database Sequence: Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		CD105862 AGENCOURT	BQ672290 AGENCOURT	BQ673186 AGENCOURT
SUMMARIES		ID	503.2 60.7 4230 11 BC063833	CD105862	BQ672290	BQ673186
		DB	177	14	13	13
		Query Match Length DB	4230		929	919
	æ	Query Match	503.2 60.7	59.5	55.4	54.4
				493.2	459.6	451
		on .	-	7	ო	4

BF074459 221883 MA BG387051 602454749 BC062931 MNB mUSCU BF388854 602046021 AU125614 AU125614 BU556872 AGENCOURT BE908201 601502458 BE90823 601502458 B1412588 602990468 CF789984 867322 MA	CB44165 655295 MA BU685298 AGENCOURT BU615520 UI H-FG0- BM69593 AG2060- AW095983 AG2060- AV696542 AG666242 CB595713 AGENCOURT BIO80524 602877005 AW911243 UE93110-Y AW911243 UE93110-Y	A13.025 MINION 602665213 B1161007 602665213 B1904605 603168411 B1526580 602255454 B1247582 602960041 BQ723.254 AGENOURT CF724654 UI-M-GZ0- BF166139 601776586 BU632049 UI-H-FE1- A1858615 W140£01.x	AGENCOU 4 6029140 7 UI-H-DT 8 X1458-10 6 6035279 6 6035279 1 VEDSOUS WYCOSOSOSOSOSOSOSOSOSOSOSOSOSOSOSOSOSOSOS
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ALIGNMENTS

RESULT 1
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HOW Sapiens CDNA clone IMAGE:6181818, containing frame-shift
ACCESSION
BC063833
BC063833 GI:39645297
KEYWORDS
HOMO Sapiens (human)
BC063833.1 GI:39645297
HOMO Sapiens (human)
BC063833.1 GI:3964528.1 HTC
BC063833.1 HTC
BC063833.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Info@bogsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandch, Anna-Lilsa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 141 Row: c Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 18765747
This clone has the following problem: frame shifted.
Location/Qualifiers
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, W.C., Rodriguez, A.C., Grimwood, J., Schmuzz, J., Myers, R.W., Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CCCGGGGCCCCGCACCACGGCTCCTACGTGCACTTCCAGCCGGCTCGCCCCACTGGTGGG 120
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                                                                                                                                                                                                                                                                            Submitted (08-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.7%; Score 503.2; DB 11; Length 4230; Best Local Similarity 77.6%; Pred. No. 3.8e-63; Matches 664; Conservative 0; Mismatches 153; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Peripheral Nervous System, dorsal root
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
Email: Gagabs-r@mail.nih.gov
Tissus Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (ILINL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                         human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
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/clone="IMAGE:6181818"
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                                                                                                                                                                                                                           Strausberg, R.
Direct Submission
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3717 AAGGACGAGCTGCTGTTTCCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCGCTG 3776
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5C_179 Homo sapiens cDNA clone
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                                                                                                   CAGGACCICTACAGCATCGTGCGCCGCCCGACCGCACCGGGGGTGCCCGTCGTCAACCTC 360
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Contact: Robert Etrausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Place: RDNA424 row: g column: 24
High quality sequence stop: 689.
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1 (bases 1 to 881)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                               361 AGGGACGAGGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTCGGGCCTCCGAGGCCCAGCTG
                                                                                                                                                                                                                                                                                                                                                       421 AAGCCCGGGGCCCGCATCTTCTTTTCGACGGCAGAGATGTCCTGCAGCACCCCGCCTGG
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IMAGE:30365831 5', mRNA sequence.
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ACCESSION
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KEYWORDS
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AUTHORS
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   /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9506"
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Eukaryota, Metasca, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metasca, Chordata, Catarrhini, Hominidae, Homo.

I (Basea I to 929)

I (Basea I to 929)

NIH-MGC http://doc.nci.nih.gov/.

Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATC

CONTA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://inage.lln.gov

Plate: LLGM2458 row: C column: 06

High quality sequence stop: 588.

BQ672290 BQ672290.1 GI:21783124 EST. Homo sapiens (human)

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:627526"
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/lab host="hH10B (bhage-resistant)"
/clone lib="NH MGC_102"
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Site_2: Ecogn; cDNA made by oligo-df priming.
Directionally cloned into EcoR1/XhoI sites using
Directionally cloned into EcoR1/XhoI sites using
the following of adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-CDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
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BQ672290 929 bp mRNA linear EST 15-JUL-2002 AGENCOURT 8354946 NIH MGC_102 Homo sapiens cDNA clone IMAGE:62752615', mRNA Sequence.

RESULT 3 BQ672290 LOCUS DEFINITION

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Conservative

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CCCTGGCGGGCAGATGACATCCTGGCCGGCCCCCGGCCTGCTGGACCCCCAGCCCTAC

421 AAGCCCGGGCCCCCATCTTTCGACGCCAGAGATGTCCTGCAGCACCCCGCCTGG 480 509 AAGCCCGGGGCCCCCCTTTAACGGCAAGACGTCCTGCAGCCCCCCCC	SULT 4 E073186 E0673186 E073186 E0786 E073186 E07318 E07318	Plate: LLCM2450 row: g column: 08 High quality sequence stop: 638. LocationQualifiers 1. 979 Corganism="Homo sapiens" /mol type="mRMA" /db_xref="taxon:9506" /clone="lkmGE:627287" /tissue type="epidermoid carcinoma, cell line" /lab_host="DHIOB (phage-resistant)" /clone=llh="NHIMGE:02287" /clone=llh="mrmafc" log: /clone=
8 6 8 6 8 6 8 6 8 6	RESULT 4 BQ673186 LOCUS LOCUS ACCESSION VERSION VERVORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOUNTAL	FEATURE SOURIGIN ORIGIN BEEL 1

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Oy 703 GCCCAC 708 Db 541 GGCAC 546	RESULT 6 BG387051 LOCUS BG387051 LOCUS BG387051 BG387051 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4582933 5', RRNA sequence. ACCESSION BG387051 LOCUS ACCESSION ACGESTION ACCESTION ACCEST	S EST. Homo sapiens (human) TSM Homo sapiens (human) TSM Homo sapiens	AUTHORS NITH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC)	COMMENT Context: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC COMMENT Library Preparation: Ling Hong/Rubin Laboratory COMMENT Tibrary Argustation: The R. Consertium (LIMI)	DIA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://inage.llml.gov	FEATURES Location/Qualifiers	source 1832 /organism="Homo sapiens" /mol_type="nRNA" / h	/clone="INAGE:4582933" /tissue_type="adenocarcinoma cell line" /tab host="nBH10B (phage-resistant)" /clone lib="NIH MGC 15"	/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:	insert size 1.8Mb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"	53.3%; Score 441.6; DE	se 550; Conservative 0; Mismatches 1 CCCTGGCGGGAGATGACATCCTGGCCGGCCCCCC	88	61 CCCGGGGCCCGCACCACGCTCCTACGTGCACTTCCAGCGGCTCGCCCCACTGGTGGG	Db 149 CCCGGAAGCCCGCACCACCAGCTCCTACGTGCACCGCGGCGCGCGACACAAG 203 Qy 121 CCCGTCCACACACCCACACCCACACAGACTTCCAGCTGGTGCTGGTGCTGGTGGTGGTGGT	Db 204CCCACCCACCGCCACCGCGACTCCCAGCCGGTGCTCCACCTGGTTGCG 255	181 CTGAACAGCCCGGGGCGGCAACCGAAGCAACCGAGGAACCGAACTTCCAATGCTTC 240	241
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle JOURNAL Genome Res. 11 (4), 626-630 (2001)	11282978 Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PD Box 166, Clay Center, NE 68933-0166, USA TEL: 402 762 4390 Fax: 402 762 4390 Email: Smith@email.marc.usda.gov	s called and all cilimed with ed by cross_match with the -mi	FORWALD: AGGARACAGITATGACCAT BACKWARD: GTITTCCAGTACGACG Plate: 81 row: F column: 9 Seq primer: ATTTAGGTGACACTATAG. Location/Qualifiers		/clone_lib="MARC_2BOV" /clone_lib="MARC_2BOV" /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,	adrenal, and endometrium." ORIGIN	Query Match 53.7%; Score 445.2; DB 10; Length 551; Best Local Similarity 88.5%; Pred. No. 7.2e-55; Matches 483; Conservative 0; Mismatches 63; Indels 0; Gaps 0;	Oy 163 GTGCTGCACCTGGTGGCCCTGAACAGCCCGCAGCCGGGGGGCATGCGAGGATCCGGGGGA 222	QY 223 GCGGACTTCCAGTGCTTCCAGCAGCGCGCGCGGGGCTGGCCGGCACCTTCCGGGCC 282 DD	Qy 283 TTCCTGTCGCGGCTGCAGGACCTCTACAGCATCGTGCGCCGGCCG	0y 343 GIGCCGICGICAACCICAAGGACGAGGIGCICTTCCCCAGGAGGCCTTATTCTCG 402	Qy 4.03 GGCTCCGAGCTGAAGCCCGGGCCCGCATCTTTTCGACGGCAGAGATGTC 4.62	463 CIGCAGCCCCGCCTGGCCCCGGAAGAGCGTGTGCCACGGCTCCGACCCCAGCGGCGCG	Db 301 CTTCAGCATCCCACTGGCCCCAGAAGAGCGTGGCACGGCTCATACCCCAGGGGGGGG	Oy 523 CGCCTGACCGACACCTACTGCGACACGCGACGGACGGACG		421	TICATIGICATCIGATCGAGAACAGCTTCATGACCTCCTCCTCCAAGTAGGGCCTCTGC

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Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Stapleron, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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Butterfield, Y. S., Krzywinski, M.I., Skalska, U., Samilus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTC 17-DEC-2003
                                                                     CAGGACCTCTACAGCATCGTGCGCGCGCCGACCGCACCGGGGTGCCCGTCGTCAACCTC 360
                                                                                                                                                                                                                 420
                                                                                                                                                                                                                                                             436 AAGGACGTGCTGCTTTCCCAGCTCGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTG 495
                                                                                                                                    421 AAGCCCGGGGCCCGCATCTTCTTTTCGACGCAGAGATGTCCTGCAGCACCCCGCCTGG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            615
316 CAGCAGGCGCGGGCCGTGGGCGGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCTG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       539 ACTGCGAGACGTGGCGGACGGAGGCCCCGGCGGCACCGGCCACGCGTCGTCGCTGCTGG 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     616 ACTGTGAGACGTGGGGGACGGAGGCTCCCTCGGACACGGCCCAGGCCTC-TCGCTGCTGG 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           599 CGGGCAGGCTGCTGGAGCAGGAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCA 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             675 GGGGCAGGCICCIGGGGCAGAGGCGGGGGCTTGCCTCACGCCTACATCGTGCTCTGCA 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 4192)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (26-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
                                                                                                                                                                                                      361 AGGGACGAGGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTCGGGGCTGCGAGGGCCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                496 AAGCCCGGGGCACGCATCTTCTCCTTTGACGGCAAGGACGTCCTGAGGCACCCCCACCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 CCCCGGAAGAGCGTGTGGGCACGGCTCCGACCCCAGCGGGCGCC--GCCTGACCGACAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    556 CCCCAGAAGAGCGTGTGGCATGGCTCGGACCCCAACGGGCCGCAGGCTGACCCGAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC062931 4192 bp mRNA linear HTC 17-DEC Mus musculus cDNA clone IMAGE:30354418, containing frame-shift
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC062931
BC062931.1 GI:38614356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGAGAACAG 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGAGAACAG 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg, R.
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TITLE
JOURNAL
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KEYWORDS
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BC062931
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: Plate: Row: Column: 0
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 13937350
This clone has the following problem: frame shifted.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3313 cécrégédadadardacarceregecaacecacededefectédeagacesecédecerase 3372
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Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,

Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,

Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,

Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CCCGGGG---CCCCGCACCACGGCTCCTACGTGCACTTCCAGCCGGCTCGCCCCACTGGT 117
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73.5%; Pred. No. 1.5e-53;
tive 0; Mismatches 192; Indels 33; Gaps
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/Lone_lib="NHE BMAP_FYO"
/lab_hose="DilloB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/dstrain="C57BL/"
/db xref="taxon:10090"
/clone="IMAGE:30354418"
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Matches 625; Conservative
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musc. I (bases 1 to 843)

Si NIH-Moch htp://mgc.nci.nih.gov/

In (bases 1 to 843)

National Institutes of Health, Mammalian Gene Collection (MGC)

Londate: Robert Strausberg, Ph.D.

Email: cgapbe-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

Contact: Robert Strausberg, The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Http://image.lln.gov

Plate: LLAMSS1 row: I column: 05

Hich mailty sequence stor. 761
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                               3841 TACTGTGAGACATGGCGAACTGAAACTACTGGGGCTACAGGTCAGGCCTCCTCCCTGCTG 3900
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/clone="IWAGE:4195660"
/lab_wade="DH10B (I phage-resistant)"
/clone lib="NCI CGAP Li9"
/note="Organ: liver; Vector: pCWV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average libert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/organism="Mus musculus"
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/strain="FVB/N"
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Best Local Similarity 77.9
Matches 547; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
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Genomics Laboratory
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/cell_type="teratocarcinoma"
/call_inne="NT2"
/clone_lib="NT2RM4"
/note="Vector: pME188FL3; mRNA from uninduced NT2 neuronal
precursor cells"
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCCTGGCGGCAGATGACATCCTGGCCGGCCCCCCCCCGCCTGCTGGACCCCCAGCCCTAC
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Best Local Similarity 82.3%; Pred. No. 4.7e-52;
                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM4001897"
                                                                                                                                                                               Helix Research Institute.
Location/Qualifiers
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                                                                         E (Manimatra) Enteresty Category (Manimatra) Manimatray (Machine 1947)

S MIH-MGC http://Mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Conteat: Robert Estrausberg, Ph.D.

Email: Gapba-r@mail.nih.gov

Tissue Procurement: ATCC

CDN Library Preparation: Rubin Laboratory

CDN Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

MA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://mage.lnl.gov

Plate: LLCM2/95 row: f column: 04

High quality sequence stop: 616.
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84.2%; Pred. No. 4.9e-52;
tive 0; Mismatches 82; Indels 13; Gaps
                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/db_xref="taxon:9606"
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EST 16-SEP-2002

BUS56872 947 bp mRNA linear ES: AGENCOURT_10186760 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:6584644 5', mRNA_sequence.

DEFINITION RESULT 10 BU556872

GGCAAGCTTCTTGGG 701

& g ठ g

GI:22907168

BUS56872

ACCESSION VERSION

Homo sapiens (human)

KEYWORDS SOURCE ORGANISM

Homo sapiens BU556872.1

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241 GCTGCTGTTTCCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGG 300
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                                                                                                               369 GGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTCGGGGCTCCGAGGCCCAGCTGAAGCCCGG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 70°)

NIH-MGC http://mgc.nci.nih.gov/.

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Produrement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llni.gov

light quality sequence stop: 688.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="TWAGE:3902175"
/tissue_type="spithelioid carcinoma"
/lab_host="hulb8 (plage-resistant)"
/clone lib="NHH MGC 70"
/note="Organ: pancreas; Vector: pCNV-SPORT6; Site 1: Not1; Ste_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1:1 kb. Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                 BE908201 707 bp mRNA linear EST 20-OCT-2000 601500458F1 NIH_MGC_70 Homo sapiens CDNA clone IMAGE:3902175 5',
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      AAGCCCGGGGCCCGCATCTTCTTTCGACGCAGAGATGTCCTGCAGCACCCCGCCTGG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                             BE908201.1 GI:10402537
EST.
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Homo sapiens
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Homo saptens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (Dases 1 to 757)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clond through the I.M.A.G.E. Consortium/LINL at:

Http://image.llnl.gov

Plate: LLAMPJO9 row; i column: 09

High quality sequence stop; 757.
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601502237F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3904208 5',
mRNA sequence.
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Bonaldo, Ph.D.

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   Library constructed by Life
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 874)
Musch Chtp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (199)
Unpublished (199)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
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                                                                                                                                              51.0%; Score 422.4; DB 1:78.8%; Pred. No. 1.5e-51;
Average insert size 1.1 kb.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM1361 row: g column: 18
Plate: LLAM1361 row: g column: 18
High quality sequence start: 23
High quality sequence scop: 808.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                         'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="mRNA"
/strain="Czech II"
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Contact: Smith TPL

Contact: Smith TPL

DSBA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4366
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I (Dases 1 to 504)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from embryos representing early developmental stages
260 GGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATCG 319
                                                                                                                               CTCCTGGAACAGAAAGCTGCGAGCTGCCACAACAGCTACATCGTCCTGTGCATTGAGAAT 670
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//mol_type="mRNA"
//db_xref="taxon:9823"
//db_host=="DH10B"
//lab_host=="DH10B"
//clone_lib="MARC_4PIG"
//note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
//note="Wade with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."
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867322 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
CF789984
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                                                                                                                                                                                               667 AGCGTCATGACCTCCTTCTCCAAGTAGGGCCGC 699
                                                                                                                                                                                                                                                                  AGCTTCATGACCTCTTTCTCCAAATAGGGCCTC 703
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al Similarity 89.0%;
446; Conservative
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Sus scrofa
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovoinae; Bovoinae; Bos.

1 (bases 1 to 657)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Tel: 402 762 4356
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with plate; FQY8051 row: I column: 11
Seq primer: TAGAAGCACAGTCGAGG.
                                                                                                                                                                                                                                                                                                                                                                                                             EST 25-MAR-2003
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                                                                                   560 AGGCCCCGGCGGCCACCGGGCAGGCGTCGTCGCTGCTGGCGGGCAGGCTGCTGGAGGAGGAG 619
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81.5%; Pred. No. 1.5e-48;
ative 0; Mismatches 105; Indels 0;
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/db xref="taxon:9913"
/tissue_type="pooled"
/tissue_type="pooled"
/lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .657
/organism="Bos taurus"
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                                                                                                                                                                                                                                                            680 CCTTCTCCAAGTAGGGCCGCG 700
                                                                                                                                                                                                                                                                                     481 CCGCCTCCAAGTAGGATCTCG 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB444165.
CB444165.1 GI:29233914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 464; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
CB444165/c
                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
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241 TCTCTTTCGACGCAGAGACGTCCTTCAGCACCCTGCCTGGCCCCAGAAGAGCGTGTGGC 300

Search completed: March 29, 2004, 14:52:44 Job time : 2570.3 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

March 26, 2004, 13:28:41; Search time 57.222 Seconds (without alignments) 1135.676 Million cell updates/sec о :: Run

US-09-938-391-2 1239 1 PWRADDILAGPPRLLDPQPY......CRHAFVVLCIENSVMTSFSK 230

Perfect score:

BLOSUM62 Scoring table: Sequence:

Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseq11980s: *
geneseqp2000s: *
geneseqp2001s: *
geneseqp2001s: *
geneseqp2001s: *
geneseqp2003s: *
geneseqp2003s: * A_Geneseq_29Jan04:* 1: genesedp1980a.* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		* Query				-	
	Score	Match	Length	8	OI .	Description	Ę.
7-	ָ ֡֡֓֞֝	100.0	230		AA017429	_	Canine pr
N	1019	82.2	275		AAU76689		Synthetic
m	1019	82.2	310		AAU76688	_	Human col
4,	1019	82.2	682		ABP41878	8	Human ova
'n	1019	82.2	1301	N	AAW92296		Human alp
φ	1019	82.2	1336		AAY08694		Human col
7	1019	82.2	1336		ABP96308	_	Human end
α	1019	82.2	1516		ABB83471		Human col
σ	1019	82.2	1516		ABP68617	_	Нишап рап
10	1003	81.0	684		AAW26327	_	Human alp
11	1003	81.0	684		AA017357	_	Human col
12	982	79.3	684		AAY25113		Human alp
13	980.5	79.1	1288		AAW26328		Mouse alp
14	976	78.8	1288		AAW92297		Mouse alp
15	996	78.0	184		AA017430	0	Canine en
16	959	77.4	184		AAY70265		Canine an
	940	75.9	684		AAY25114		Mouse alp
18	869	70.1	195		AAW90874	_	Human HMW
	868	70.1	193		AAW90877	~	Human HMW
20	850	68.6	184		ABG31794		Murine en
21	843	68.0	191		AAB28398	_	Murine en
22	843	68.0	191		AAU77950		Amino aci
23	838.5	67.7	271		AAB08407	Aab08407 A	ю
24	836	67.5	216		AAB30495		
	835	67.4	181	4	AAU00898	Aau00898 H	Human End

2 Human	Aay94323 Human end	Aab28399 Human end	Aau00897 Human End	Aau77951 Amino aci	Aay02113 SEQ ID 76	Aay08693 Human end	2 Human	1 Human	Aab16451 Human end	3 Amino	Aab49379 Human end	Aau00896 Human End	Abb79901 Human end	Aam49503 Human end	Aam48895 Human end	Aau97132 Human end	Aag79753 Human end	Human	Aau00899 Human End
AAY59622	AAY94323	AAB28399	AAU00897	AAU77951	AAY02113	AAY08693	AAY70252	AAY90771	AAB16451	AAB30493	AAB49379	AAU00896	ABB79901	AAM49503	AAM48895	AAU97132	AAG79753	ABG73586	AAU00899
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182	182	182	182	182	183	183	183	183	183	183	183	183	183	183	183	183	183	513	180
67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.3
835	835	83.5	835	835	835	835	835	835	835	835	835	835	835	835	835	835	835	835	834
56	27	20	50	30	31	35	33	34	3	36	37	- 60 - M	6	40	41	2 7	43	44	45

ALIGNMENTS

AA017429 standard; protein; 230 AA. (first entry) 19-JUL-2002 AA017429; RESULT 1 AAO17429

Canine pro-endostatin.

Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriamis; rheumatoid arthritis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasha; tubosis; olser-webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; angiofibroma; wound granulation; coronary collateral; collateral; arteriovenous malformation; escrebral collateral; arteriovenous malformation; decrebral angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiathritic; antipsoriatic; antidiabetic; ophthalmological; gynaecological.

Canis familiaris.

EP1191036-A2.

27-MAR-2002.

24-AUG-2001; 2001EP-00307224.

25-AUG-2000; 2000US-0227924P.

(PFIZ) PFIZER PROD INC

Sheppard MG, Tong X;

WPI; 2002-354068/39 N-PSDB; AAL46062.

An isolated nucleic acid molecule for the treatment of angiogenesis-related disorder, such as cancers or diabetic retinopathy, encodes an endostatin protein.

Claim 14; Fig 3; 56pp; English.

The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration,

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                                rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovasculariaation, telangiectasia, haemophillac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine pro-endostatin protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 INSPOPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LNSPOPGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLODLYSIVRRADRTGVPVVNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 RDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 RDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PWRADDILAGPPRILIDPOPYPGAPHHGSYVHFOPARPIGGPVHTHTHTHODFOLVLHLVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PWRADDILAGPPRLLDPQPYPGAPHAGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i. .19
/note= "Encoded by mouse Ig signal peptide (mIgSP) exon"
   graft rejection, neovascular glaucoma, retrolental fibroplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; Ig signal peptide; mIgSP, functional protein domain; FPD; primary translational product; PTP; DNA construct; regulatory DNA; DNA targeting segment; regulatory factor; single regulatory unit; monoclonal antibody; recombination-derived alteration; blood product; human; COL18A1; mutant; mutein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CETWRIBAPAAIGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMISFSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CETWRTEAPAATGQASSLLAGRILEQEAASCRHAFVVLCIENSVWTSFSK 230
                                                                                                                                                                                                                                                                                                                                      ; Score 1239; DB 5; Length 230;
; Pred. No. 3.2e-131;
0; Mismatches 0; Indels 0;

    19
/label= Signal peptide
/note= "Mouse Ig signal peptide (mIgSP)"
/note= "Mouse Ig signal peptide (mIgSP)"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20. .275
/label= Mature human COL18A1 protein"
/note= "Contains exons 38-41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV. (CHAP/) CHAPMAN P W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU76689 standard; protein; 275 AA.
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 230; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-2001; 2001WO-GB003455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-2000; 2000GB-00018876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                     Sequence 230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
Synthetic.
Chimeric.
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   corneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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AAU76689
ID AAU7
XX
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DT 21-M
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The present invention relates to a new method of producing a protein, and the present inventional protein domain, that is either C- or N-terminus of the puch as functional protein domain, that is either C- or N-terminus of the privary translational product (PTP) of a gene, where the profein has beloaded a regular tory DNA and a DNA targeting segment. This method is comprising a regularory DNA and a DNA targeting segment. This method is useful for producing a functional protein domain of proteins such as regularory blood products and monoclonal antibodies. The method described in the invention allows controlled and precise modification of the host cell genome in order to produce functional protein domain (FPD). The amount of exogenous sequence to be integrated in the host cell genome itself is used. Use of the host cell genome itself is used. Use of the host cell sequence encoding sequence, the original coding sequence present in the host cell genome itself is used. Use of the host cell sequence encoding sequence, the original coding sequence can also making use of the same post-transcriptional (e.g., splicing) and/or post-translational (e.g., splicing) processes that are complementary but coding for the maturation of FPD. The use of a single complementary but coding for the maturation of FPD. The use of a single complementary but coding for the expression vector. The present amino acid sequence represents the plasmid pEnd-HR#1 FPD fusion protein of the invention. This fusion protein contains the mouse Ig signal peptide in two forms as 4.1 of the human COLIBAL sequence (mIGSP) sequence tused to exone 38-41 of the human COLIBAL sequence
                                                                                                                       Producing functional protein domain by growing host cell transfected with DNA construct having regulatory DNA and DNA targeting segment, and optionally culturing homologously recombinant cell and collecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDEVLFPSWEALFSGSEGQLKFGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 KDELLFPSWEALFSGSEGPLKFGARIFSFDGKÖVLRHFTWPOKSVWHGSDPNGKRLTBSY 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PWRADDILAGPPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNSPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSIVRRADRAAVPIVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.2%; Score 1019; DB 5; Length 275; Best Local Similarity 82.4%; Pred. No. 3.1e-106; Matches 187; Conservative 16; Mismatches 20; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CETWRIEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMTS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CETWRTEAPSATGQASSLLGGRILIGOSAASCHHAYIVLCIENSPMTA 273
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  Falciola L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU76688 standard; protein; 310 AA.
                                                                                                                                                                                                                                                        Example; Fig 8; 116pp; English.
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  De Luca G,
                                                  2002-195963/25.
                                                                        N-PSDB; ABK09977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 275 AA;
Chapman PW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-2002
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                                                                                                                                                                                                        protein.
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us-09-938-391-2.rag

4;

Indels

Pred. No. 3.7e-106; ; Mismatches 20;

al Similarity 82.4%; Pr 187; Conservative 16;

Local Best Loca Matches

```
monoclonal antibody; recombination-derived alteration; blood product
                                                                      /label= Hinge_region
/note= "Encoded by exon 38"
117. 310
/label= Endostatin_core_domain
/note= "Autonomous folding unit"
                             1. .54
/label= Multimerisation_domain
                                                                                                  137. .201
/note= "Encoded by exon 39"
202. .241
                                              "Encoded by exon 36"
                                                     44. .54
/note= "Encoded by exon 37"
                                                                                                                202. .241
/note= "Encoded by exon 40"
                                                                                                                                   note= "Encoded by exon 41"
                                                                                                                                                                                               (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV. (CHAP/) CHAPMAN P W.
                                                                                                                                                                                                                  Falciola L;
                       location/Qualifiers
                                                                                                                                                                                    01-AUG-2000; 2000GB-00018876
                                                                                                                                                                        01-AUG-2001; 2001WO-GB003455
                                                                                                                             .310
                                                                 55. .136
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                                          1. .43
/note=
                                                                                                                                                                                                                  Chapman PW, De Luca
                                                                                                                                               WO200210372-A1
            Homo sapiens
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Producing functional protein domain by growing host cell transfected with DNA construct having regulatory DNA and DNA targeting segment, and optionally culturing homologously recombinant cell and collecting protein. WPI; 2002-195963/25.

Example; Fig 3; 116pp; English.

The present invention relates to a new method of producing a protein, such as functional protein domain, that is either C or N-terminus of the primary translational product (PTP) of a gene, where the protein has biological activity which is distinct from PTP. The method of the invention involves growing a host cell transfected with a DNA construct comprising a regulatory DNA and a DNA targeting segment. This method is useful for producing a functional protein domain of proteins such as regulatory factors, blood products and monoclonal antibodies. The method described in the invention allows controlled and precise modification of the host cell genome in order to produce functional protein domain (FPD). The amount of exogenous sequence to be integrated in the host cell genome is used. Use of the host cell genome is every limited since, as coding sequence, the original coding sequence present in the host cell genome itself is used. Use of the host cell genome tiself is used. Use of the host cell genome treation of such ording sequence are encoding FPD also provides the advantages of both eliminating making use of the same post-transcriptional (e.g., splicing) and/or post-translational (e.g., splicing) and or post-translational (e.g., splicing) and or post-translational (e.g., splicing) and or complementary but coding for the maturation of FPD. The use of a single regulatory unit eliminates the necessity of manipulating the complementary but coding for the EPPD and adapt it to the expression vector. The segment coding for the FPD, and coding for the protein domain used to illustrate the method of the invention

Sequence 310 AA;

Query Match

Length 310; 5. <u>B</u> 82.2%; Score 1019;

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86 PWRADDILASPPRLPEPQPYPGAPHHSSYVHLRPARPTSPP----AHSHRDFQPVLHLVA 141
                                                                                             61 INSPOPGGMRGIRGADFOCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRIGVPVVNL 120
                                                                                                                          261
                                                                                                                                                                                               121 RDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; pcos; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; antibody preparation; cytostatic; immunoadulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; chromosome 21q22.3.
                                                                                                                                                                                                                       202 KDELLFPSWEALFSGSEGFLKFGARIFSFDGKDVLRHPTWPQKSVWHGSDPNGRRLTESY
1 PWRADDILAGPPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVA
                                                                                                                                                                                                                                                                                            Human ovarian antigen HEEBK29, SEQ ID NO:3010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP41878 standard; protein; 682
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Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases. The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polymuclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen of polymuclectides, antibodies against human ovarian antigens, and the use of ovarian antigen polymuclectides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related Claim 11; SEQ ID NO 3010; 2922pp; English. WPI; 2002-147878/19. N-PSDB; ABQS4955.

disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatorry conditions (e.g., mascritis, ophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood related disorders (e.g., ansemia), cardiovasoular disorders, cepticatory disorders and used also be used in screening for compounds which modulate ovarian antigen by pression or activity. The polymucleotides may further be used for gene therapy, chromosome mapping, in the conflict dentification of individuals and in forensic analysis, and the polymorleotides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequence

Sequence 682 AA;

513 120 573 RDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY 180 633 9 1 PWRADDILAGPPRILDPOPYPCAPHHGSYVHFOPARPIGGPVHTHTHTHODFOLVLHLVA LINSPOPGGMRGIRGADFOCFODARAAGLAGTFRAFLSSRLQDLYSIVRRADRIGVPVVNL 514 İNSPLSGGMRGİRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSIVRRADRAAVPIVNL 82.2%; Score 1019; DB 5; Length 682; 82.4%; Pred. No. 1.1e-105; tive 16; Mismatches 20; Indels ' CETWRIEAPAAIGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMTS 227 Query Match Best Local Similarity 82.4[§] Matches 187; Conservative 61 121 181 Ś g ò 셤 ð 셤 ò ద

AAW92296 standard; peptide; 1301 AA. 28-APR-1999 AAW92296; RESULT

(first entry)

Human alpha-1 (XVIII) collagen chain common sequence HU18(common)36.

Human; type XVIII collagen; liver disease; cirrhosis; detection; hepatocellular carcinoma; diagnosis.

Homo sapiens

17-DEC-1998.

98WO-US012327. 12-JUN-1998;

97US-0049369P. 12-JUN-1997; (FIBR-) FIBROGEN INC. (FIFI-) ACAD FINLAND. (INRM) INST NAT SANTE & RECH MEDICALE.

Clement B; Rehn M, Pihlajaniemi T,

WPI; 1999-070292/06.

Diagnosis and monitoring of liver disease by measuring collagen type XVIII levels - with elevated levels indicative of disease, especially cirrhosis or hepatocellular carcinoma.

Example 6; Fig 8; 56pp; English

A method has been developed for the detecting liver disease. The method comprises: (a) reacting a patient sample with antibodies (Ab) specific for collagen type XVIII (coll8); (b) measuring the amount of Ab-antigen complex (C) formed as indicator of the amount of Coll8 present; (c) similar analysis of a non-diseased control; and (d) comparing the amounts of Coll8 in the two samples to detect presence or progression of disease. Elevated levels of Coll8 are: (i) indicative of disease, specifically cirrhosis; and (ii) predictive of the prognosis of disease, specifically hepatocellular carcinoma (there is a relationship between Coll8 mRNA levels and tumour size and necrosis, and survival times are significantly higher in patients with higher Coll8 levels). The method provides non-livasine, early and accurate diagnosis of liver disease. The present sequence represents the sequence common to human alpha-1 (XVIII) collagen chain from the present invention

Sequence 1301 AA;

9 ., Length 1301; 82.2%; Score 1019; DB 2; Length 130 82.4%; Pred. No. 2.9e-105; tive 16; Mismatches 20; Indels Best Local Similarity 82.48 Matches 187; Conservative Query Match

1192 1077 PWRADDILASPPRLPEPQPYPGAPHHSSYVHLRPARPTSPP----AHSHRDFQPVLHLVA 1132 LNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNL 1 PWRADDILAGPPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHQDFQLVLHLVA RDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY 121 61 g ò 셤 à 원

CETWRIEAPAATGQASSLIAGRILEQEAASCRHAFVVLCIENSVMTS 181 1253

ઠ ద AAY0869

AAY08694 standard; protein; 1336 AA

AAY08694;

10-AUG-1999 (first entry)

Human collagen 18 protein.

Plasminogen; human; angiostatin; endostatin; gene therapy; vector; anti-angiogenic; attenuation; cytostatic; anti-diabetic; ophthalmology; tumour growth; solid tumour; diabetic retinopathy; retina; collagen 18.

Homo sapiens

WO9926480-A1

03-JUN-1999.

98WO-US024950. 20-NOV-1998;

97US-00975424.

(GENE-) GENETIX PHARM INC. (MASI) MASSACHUSETTS INST TECHNOLOGY.

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Disclosure; Page 77-80; 83pp; English
                             Anti-angiogenic gene therapy vectors
                                                                                                                                                                                                                                             ABP96308 standard; protein; 1336 AA
    Bachelot
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                                                                                                                                                                                                                                                                 (first entry
    Leboulch P, Pawliuk RJ,
                                                                                                                                                                                                                                                                           Human endostatin protein
             WPI; 1999-357696/30.
N-PSDB; AAX77720.
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1168 LNSPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSIVRRADRAAVPIVNL 1227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1228 KDELLFPSWEALFSGSEGPLKFGARIFSFDGKDVLRHPTWPQKSVWHGSDPNGRRLTESY 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LNSPOPGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLODLYSIVRRADRIGVPVVNL 120
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                                                                                                                                                 The present invention describes a humanised baculovirus (I) which comprises a modified baculovirus genome having a nucleic acid molecule encoding a therapeutic agent and a polypeptide which functions to target the baculovirus to at least one cell type. Also described is a not an be used in gene therapy. The baculovirus is useful in the manufacture of a medicament for the treatment of cancer, particularly protein, which is specified in the exemplification of the present sequence represents the human endostatin protein, which is specified in the exemplification of the present invention. N.B. The present sequence is not given in the specification but is referred to in Claim 24 as Genbank accession number NM_130445
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                                  New baculovirus having a modified genome encoding a therapeutic agent, useful in the manufacture of a medicament for the treatment of cancer, particularly prostate cancer.
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/note= "This region is specifically claimed in Claim
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                                                                                                                     Claim 24; Page; 34pp; English.
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Best Local Similarity 82.4%
Matches 187; Conservative
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WPI; 2003-268336/26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel viral gene therapy vector comprising a nucleic acid molecule encoding an anti-anglogenic polypeptide chosen from human or murine encoding an anti-anglogenic polypeptide chosen from inhibiting fusions and fragments, where the viral vector is sufficiently attenuated for use in human gene therapy. The products of the invention activity. The vector is used in gene therapy for inhibiting tumour growth in humans harbouring a solid tumour. The vector expresses an anti-anglogenic pypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-anglogenic polypeptide inhibits anglogenesis in the vicinity of the retina. The vector is administered to cells ex vivo and then administered to the patient
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Hepler WT, Jiang Y;

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WPI; 2002-583596/62.
N-PSDB; ABN85301.
                                                      Sequence 1516 AA;
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12-JUL-2001;
20-AUG-2001;
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21-MAR-2001;
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The invention relates to an isolated polymucleotide (1) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences consisting of at least 20 contiguous complements of (a); (d) sequences that hybridize to (a), under moderately to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596 to (a) a patient conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596 to any abtient and compositions comprising polypeptides (ABP68596 to any attient and compositions comprising polypeptides to presenting calls between the polypeptide are useful in treating penceatic cancer and simulating an immune response. The polymucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly verver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1348 INSPLSGOMRGIRGADFOCFOQARAVGLAGTFRAFLSSRLODLYSIVRRADRAVFIVNL 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1292 PWRADDILASPPRLPEPQPYPGAPHHSSYVHLRPARPISPP----AHSHRDPQPVLHLVA 1347
                                                                                                                 New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 INSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PWRADDILAGPPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHQDFQLVLHLVA
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                                                                                                                                                                                                            Claim 2; SEQ ID NO 166; 300pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.2%; Score 1019; DB 5;
82.4%; Pred. No. 3.6e-105;
ive 16; Mismatches 20;
  Persing DH,
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/label= GXYGX'Y'_motif
/nnte= "Claim 1"
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/label= GXYGX'Y'_motif
/note= "Claim 1"
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Lodes MJ,
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Best Local Similarity 82.4%
Matches 187; Conservative
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Kalos MD,
                                              WPI; 2002-627435/67.
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                                                                     N-PSDB; ABV94763
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Benson DR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 RDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY 180
                                                                                                                                                                                                                              comprising a DNA encoding an anti-anglogenic protein, which shows therapeutic effects on rheumatoid arthritis. The composition is useful for treating rheumatoid arthritis and the gene therapy is effective, lasting for 14 days. The present sequence is the protein sequence for human collagen XVIII. Endostatin, which consists of the C-terminal 183 residues of collagen XVIII, was used as an anti-anglogenic protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
                                                                                     Novel composition for gene therapy against rheumatoid arthritis, comprising a DNA encoding anti-angiogenic protein or its parts.
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cytostatic; tumour,
                                                                                                                                                                                                    The present invention relates to a composition for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                               82.2%; Score 1019; DB 5; Length 1516; 82.4%; Pred. No. 3.6e-105; ive 16; Mismatches 20; Indels 4
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                                                                                                                                                        Claim 4; Page 70-78; 84pp; English.
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; 2001US-0265682P.
; 2001US-0267568P.
; 2001US-0278651P.
; 2001US-0291631P.
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Matches 187; Conservative
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4; Gaps

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Length 1516;

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| Jobel = GXYGX'Y' motif |
| Jabel = GXYGXYY' motif |
| Jabel = GXYGYYY' mo Peptide

Nucleic acid encoding human alpha-1 collagen - for production of recombinant alpha-1 collagen, for use in the treatment of cartilage Claim 1; Col 23-30; 35pp; English. 93US-00159784. 93US-00159784 (HARD) HARVARD COLLEGE WPI; 1997-350247/32. N-PSDB; AAT84484. oh SP; degeneration. 01-DEC-1993; 01-DEC-1993; US5643783-A. Olsen BR,

Novel human type alpha-1 (XVIII) collagen is characterised by 10 triple helical domains containing the GXYGX'Y' motif (where X, Y, X' and Y' represent any amino acid), the helical domains being separated and flanked by non-triple helical regions which may provide flexibility. Alpha-1 collagen is expressed in multiple tissues, especially liver, lung and kidney. A claimed plasmid comprising alpha-1 collagen nucleic acid (see AAT84484) and an expression control sequence can be used to express recombinant collagen in prokaryotic or eukaryotic (especially mammalian) host cells. The alpha-1 collagen may be used to treat a patient suffering from a disease associated with cartilage degradation, and for supplementing collagen. It can also be used as a connective tissue filler (e.g. for plastic surgery), can be interposed between a dermal equivalent

1 PWRADDILAGPPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVA 60 Query Match
Best Local Similarity 81.5%; Pred. No. 7.4e-104;
Matches 185; Conservative 15; Mismatches 23; Indels 4; Gaps

575 RDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY 180 LNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNL 120 61 121 qq 8 6 셤 ઠ

181 CETWRIEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVWTS 227

AA017357 standard; protein; 684 AA AAO17357;

(first entry) 19-JUL-2002

Human collagen type XVIII alpha 1.

Human, endometriosis; DNA chip; fibronectin; p27; reticulocalbin; aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin; insulin-like growth factor binding protein-2; alpha-2 type IV collagen; transmembrane receptor PTK7; collagen type XVIII alpha 1; platelet derived growth factor receptor alpha; laminin M chain; subtilisin like protein PACE4; nidogen.

Homo sapiens. EP1191107-A2

27-MAR-2002.

21-AUG-2001; 2001EP-00250300.

25-SEP-2000; 2000DE-01048633

(SCHD) SCHERING AG

m Winterhager œ, Kreft Kraetzschmar J, ď, Hess-Stumpp H, Haendler Regidor P, Scotti S;

WPI; 2002-317413/36.

In vitro diagnosis and monitoring of endometriosis, comprises detecting reduced expression of specific gene products, e.g. from the fibronectin

Claim 1; Page 12-13; 21pp; German.

The present invention relates to a method for the in vitro diagnosis of endometriosis by determining the amount of gene product from at least one specific gene in a patient sample and comparing this with the amount of gene product in a patient sample and comparing this with the amount of endometriosis. The gene products may be fibronectin, p27, reticulocalbin, albulin-like growth factor binding protein-2, alpha-2 type IV collagen, transmembrane receptor PRTA, collagen type XVIII alpha 1, platelet transmembrane receptor receptor alpha, laminin M chain, subtlisin like protein PACE4 or nidogen. The method is useful for initial diagnosis of endometriosis, and also for monitoring progress and treatment of the disease. The present sequence is human collagen type XVIII alpha 1

Sequence 684 AA;

4; Gaps Query Match

81.0%; Score 1003; DB 5; Length 684;
Best Local Similarity 81.5%; Pred. No. 7.4e-104;
Matches 185; Conservative 15; Mismatches 23; Indele

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RDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY 180 121

CETWRIEAPAAIGOASSLLAGRILEOEAASCRHAFVVLCIENSVMIS 227 181

AAY25113 standard; protein; 684 AA (first entry) 25-AUG-1999 RESULT 12
AAY25113
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Human alphal (XVIII) collagen protein.

Alphal(XVIII) collagen; mimetic; endostatin; atomic coordinate; library; anti-angiogenic; heparin binding domain; receptor binding domain; mimic; alpha-helix A domain; carbohydrate recognition domain; CRD domain;

#OOP KT:75:/T K7 JEW GOW

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Mouse alpha-1 collagen (XVIII)
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/label= GX
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/label= GX
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/label= GX
315. .320
/label= GX
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/label= GX
337. .342
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/label= GX
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'label= GX
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/label= GX
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This invention describes a novel method for identifying mimetics of mammalian endostatin. The method comprises identifying a compound having atomic coordinates with non-trivial similarity to selected coordinates of atomic coordinates of atomic coordinates of atomic coordinates of atomic coordinates of atomic coordinates of atomic coordinates of compounds in a library of candidate compounds, (b) comparing the library of atomic coordinates of a mammalian endostatin and (c) selecting from the library at least one candidate compound on the basis of selection criteria which include similarities between the atomic coordinates of the selected candidate compound and the atomic coordinates of the mammalian endostatin. The invention also describes the use of an anti-angiogenic fragment of endostatin comprising a domain selected from a heparin binding domain, are receptor binding domain, and exposed on alpha helix A domain, and a carbohydrate recognition domain (CRD) domain. The methods can be used for designing and and selecting endostatin mimics. The compounds identified can be used for treating undesired angiogenesis, e.g. tumours. This sequence the second process of the compounds identified can be used for treating undesired angiogenesis, e.g. tumours. This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 79.3%; Score 982; DB 2; Length 684; Best Local Similarity 81.1%; Pred. No. 1.7e-101; Matches 185; Conservative 15; Mismatches 22; Indels
                                                                                                                                                                                                Identifying mimetics of mammalian endostatin.
                                                                                                                                               Sasaki
   treatment; angiogenesis; tumour; human.
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                                                                                                                           (HARD ) HARVARD COLLEGE
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                        Homo sapiens.
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Alpha-1 collagen; type XVIII collagen; cartilage degeneration.
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1237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 ALNSPOPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRIGVPVVN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PWRADDILAGPPRLLDPQPYPGAP-HHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.1%; Score 980.5; DB 2; Length 1288; Best Local Similarity 79.7%; Pred. No. 6.3e-101; Matches 184; Conservative 19; Mismatches 23; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding human alpha-1 collagen - for production of recombinant alpha-1 collagen, for use in the treatment of cartilage degeneration.
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(Jabel= GXYGX'Y' motif
897...902
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903...908
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911...916
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/label= GXYGX'Y'_motif
1145. .1150
/label= GXYGX'Y'_motif
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/label= GXYGX'Y'_motif
label gxygx'y' motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 2; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                  93US-00159784.
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N-PSDB; AAT84485.
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RESULT 14 AAW92297 ID AAW92297 standard; peptide; 1288 AA. us-09-938-391-2.rag

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Mouse alpha-1 (XVIII) collagen chain common sequence MO18(common)28.
                                         Human, type XVIII collagen, liver disease, cirrhosis, detection, hepatocellular carcinoma, diagnosis.
                                                                                                                        (FIBR-) FIBROGEN INC.
(PIFI-) ACAD FINLAND.
(INRM ) INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                 Pihlajaniemi T, Rehn M, Clement
                                                                                                98WO-US012327
                                                                                                            97US-0049369P
                 (first entry)
                                                                                                                                                             WPI; 1999-070292/06.
                 28-APR-1999
                                                                                                 12-JUN-1998;
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                                                                        409856399-A1
                                                                                    17-DEC-1998
      AAW92297;
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A method has been developed for the detecting liver disease. The method comprises: (a) reacting a patient sample with antibodies (Ab) specific for collagen type XVIII (Coll8); (b) measuring the amount of Ab-antigen complex (C) formed as indicator of the amount of Coll8 present; (c) similar analysis of a non-diseased control, and (d) comparing the amounts of Coll8 in the two samples to detect presence or progression of disease. Elevated levels of Coll8 are: (i) indicative of disease, specifically hepatocellular carcinoma (there is a relationship between Coll8 mRNA levels and tumour size and necrosis, and survival times are significantly higher in patients with higher Coll8 levels). The method provides noninvasive, early and accurate diagnosis of liver disease. The present sequence represents the sequence common to mouse alpha-1 (XVIII) collagen Diagnosis and monitoring of liver disease by measuring collagen type XVIII levels - with elevated levels indicative of disease, especially cirrhosis or hepatocellular carcinoma. chain from the present invention Example 6; Fig 8; 56pp; English

78.8%; Score 976; DB 2; Length 1288; 79.7%; Pred. No. 2e-100; ive 20; Mismatches 21; Indels 6 Best Local Similarity 79.7 Matches 184, Conservative Sequence 1288 AA; Query Match

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1117 28 1062 PWRADDILANPPRLPDPQPYPGVPHHASSYVHLPRPARPT----LSLAHTHQDFQPVLHL 1 PWRADDILAGPPRLLDPQPYPGAP-HHGSYVHF-QPARPTGGPVHTHTHQDFQLVLHL VALNSPOPGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLODLYSIVRRADRIGVPVV 59 음 ò 셤

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Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; ruboesis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; angiofibroma; wound granulation; coronary collateral; escharal; arteriovenous malformation; ischaemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; gynaecological. An isolated nucleic acid molecule for the treatment of angiogenesis-related disorder, such as cancers or diabetic retinopathy, encodes an endostatin protein. AAO17430 standard; protein; 184 24-AUG-2001; 2001EP-00307224. 25-AUG-2000; 2000US-0227924P. (PFIZ) PFIZER PROD INC WPI; 2002-354068/39. N-PSDB; AAL46063. 19-JUL-2002 (first Canine endostatin. Canis familiaris. Sheppard MG, EP1191036-A2. 27-MAR-2002 AAO17430; AA017430
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The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosts of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, nubosais, obler whebber Syndrome, wyocardial angiogenesis, plaque neovascularisation, telangiectusia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, isohaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine pro-endostatin protein sequence Claim 14; Fig 5; 56pp; English.

47 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLODLYSI 0; Gaps Length 184; 0; Indels Ouery Match
78.0%; Score 966; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 1.7e-100;
Matches 184; Conservative 0; Mismatches 0;

Sequence 184 AA;

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RESULT

1238

227 SFSK 230 |||| 181 SFSK 184 දු දු

Search completed: March 26, 2004, 13:35:56 Job time : 60.2222 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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March 26, 2004, 13:34:07 ; Search time 18.3333 Seconds
(without alignments)
647.671 Million cell updates/sec
OM protein - protein search, using sw model
                                                       Run on:
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US-09-938-391-2 1239 Title: Perfect score:

1 PWRADDILAGPPRLLDPQPY......CRHAFVVLCIENSVMTSFSK 230 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

389414 seqs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	13 Sequence 13, Appl	3 Sequence 13,	13 Sequence 13,	Sequence 13,	13 Sequence 13,	Sequence 2,	14 Sequence 14,	14 Sequence 14,	3 Sequence 3,	14 Sequence 14,	14 Sequence 14,	14 Sequence 14,	Sequence 2,	Sequence	6 Seguence 36,	Sequence 3,	-10 Sequence 10,	-11 Sequence 11,	2 Sequence 2	Sequence 2	7 Seguence 7	S	-25533 Sequence 25	'n	-27326 Seguence 2732	-19085 Seguence 1	-23421 Seguence 2342
D	US-09-561-500-	US-09-561-108-	US-09-561-526-	,	8-866-60-	US-08-159-784-	US-09-561-500-	-09-561-	US-09-315-689-	US-09-561-526-	US-09-561-499-	US-09-998-831-	39-20	9-312-6	36-80	-08-15	9-231-	US-09-231-077D	US-09-046-985-	-09-474	US-09-046-985-	US-09-474-743-	US-09-252-991A	US-09-385-442-	-09-252-991A	~09-252-991A	US-09-252-991A
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Score	843	843	843	843	843	839	835	835	835	835	835	835	835	817	790	513	195.5	œ	148	4	0	101			96	94.5	93
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Sequence 28358, A Sequence 284, Appl Sequence 22377, A Sequence 19702, A Sequence 17206, A Sequence 17, Appl Sequence 1788, A Sequence 1788, A Sequence 1788, A Sequence 1788, A Sequence 177, Appl Sequenc	
US-09-252-991A-28358 US-09-252-991A-22537 US-09-252-991A-22537 US-09-252-991A-19702 US-09-252-991A-19702 US-09-252-991A-19702 US-09-262-991A-17206 US-09-252-991A-17806 US-09-252-991A-17806 US-09-252-991A-17806 US-09-252-991A-17806 US-09-252-991A-17806 US-09-252-991A-17806 US-09-252-991A-17806 US-09-252-991A-17806 US-09-262-991A-17806 US-09-262-991A-17806 US-09-307-794A-177 US-09-307-778A-177 US-09-307-778A-177 US-09-307-778A-177	
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 KSVWHGSDPSGRRLTDSYCETWRTBAPAHGQASSLLAGRLEQBAASCRHAFVVLCIEN 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/09561500
| Fatent No. 6342210
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Philip E. Thorpe
| APPLICANT: Rolf A. Brekken
| APPLICANT: Rolf A. Brekken
| APPLICANT: Rolf A. Brekken
| TILLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
| FILE REFRENCE: 4001.002500
| CURRENT APPLICATION NUMBER: 40799/561,500
| CURRENT PLING DATE: 2000-04-28
| PRIOR PLING DATE: 1999-04-28
| NUMBER OF SEQ ID NOS: 44
| SOUTHARR: PATENTING VEGET 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 HHHHHTHQDFQPVLHLVALNTPLSGGRRGIRGADFQCFQQARAVGLSGTFRAFLSSRLQD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 68.0%; Score 843; DB 4; Length 191; Best Local Similarity 83.0%; Pred. No. 5.6e-87; Matches 156; Conservative 17; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-561-108-13
Sequence 13, Application US/09561108
Patent No. 644221
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 SVMTSFSK 230
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US-09-561-500-13
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163 KSVWHGSDPSGRRITDSYCETWRTBAPATGQASSLLAGRILLBQBASGRHAFVVLCIEN 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 83.09
Matches 156; Conservative
                                                                                                223 SVMTSFSK 230
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US-09-998-831-13
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APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REPRENCE: 4001.002584
CURRENT APPLICATION NUMBER: US/09/561,108
CURRENT APPLICATION NUMBER: 06/0-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN Ver. 2.0
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US-09-561-526-13
US-09-561-526
Sequence 13, Application US/09561526
Federation 0. 6416758
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
TITLE OF INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
FILE REFRENCE: 4001.00258
CURRENT APPLICATION NUMBER: US/09/561,526
CURRENT FILING DATE: 2000-04-28
FRIOR APPLICATION NUMBER: 60/131,432
FRIOR APPLICATION NUMBER: 60/131,432
NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 HTHTHTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 LYSIVRRADRGSVPIVNLKDEVLSPSWDSLFSGSQGQLQPGARIFSFDGRDVLRHPAWPQ 123
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                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-09-561-108-13
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match 68.0%; Score 843; DB 4; Length 191; Best Local Similarity 83.0%; Pred. No. 5.6e-87; Matches 156; Conservative 17; Mismatches 15; Indels
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LENGTH: 191
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64 LYSIVRRADRGSVPIVNLKDEVLSPSWDSLFSGSQGQLQPGARIFSFDGRDVLRHPAWPQ 123
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Sequence 13, Application US/09561499

Factor No. 6524893

GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: ROLf A. Brekken

TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF

FILE REFERENCE: 4001.025582

CURRENT APPLICATION NUMBER: US/09/561,499

CURRENT FILING DATE: 2000-04-28

FRIOR PILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 13
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Sequence 13, Application US/09998831

Patent No. 6676941

GENERAL INFORMATION:

APPLICANT: Philip B. Thorpe

APPLICANT: Rolf A. Brekken

TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY

TITLE OF INVENTION: ANTIBODY CONJUGATE CONJUGATE COMPOSITIONS FOR SELECTIVELY

TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY

TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY

TITLE OF INVENTION: ANTIBODY CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUGATE CONJUG
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154 VIQHPAWPRKSVWHGSDPSGRRITDSYCETWRTEAPAATGQASSILAGRILEQEAASCRH 213
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US-09-561-500-14
US-09-561-500-14
US-09-561-500-14
Sequence 14, Application US/09561500
Faquence 14, Application US/09561500
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
FILE REPERENCE: 4001.002500
CURRENT APPLICATION NUMBER: US/09/561,500
CURRENT APPLICATION NUMBER: 05/09/561,500
CURRENT PILING DATE: 2000-04-28
FRIOR APPLICATION NUMBER: 60/131,432
FRIOR APPLICATION NUMBER: 60/131,432
FRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 444
SOFTWARE: PatentIn Ver. 2.0
3 PARPT----LSLAHTHQDFQPVLHLVALNTPLSGGMRGIRGADFQCFQQARAVGLSGTFR
                                                                94 AFLSSRLQDLYSIVRRADRTGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRD
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-561-500-14
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ORGANISM: Artificial Sequence
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US-09-561-108-14
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LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                       163 KSVWHGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIEN 222
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                             ) OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-09-998-831-13
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                                                                                         Ouery Match 68.0%; Score 843; DB 4; Length 191; Best Local Similarity 83.0%; Pred. No. 5.6e-87; Matches 156; Conservative 17; Mismatches 156; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08159784
Patent No. 5643783
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 222 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BM PS/2 Model 50z or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
FILING DATE: December 1, 1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFRENCE/DOCKET NUMBER: 0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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STATE: Massachusetts
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STRANDEDNESS: N/A
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GENERAL INFORMATION:
Patent No. 634221
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REPERENCE: 4001.002584
CURRENT APPLICATION NUMBER: 02/09/561,108
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432
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                                                                                                                                   47 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI
                                                     0; Gaps
Query Match 67.4%; Score 835; DB 4; Length 182; Best Local Similarity 85.1%; Pred. No. 4.1e-86; Matches 154; Conservative 14; Mismatches 13; Indels
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227 S 227 181 A 181 US-09-561-526-14 FEATURE: ద à ద ઠે g 61 VRRADRAAVPIVNLKDELLFPSWEALFSGSEGPLKPGARIFSFDGKDVLRHPTWPQKSVW 120 47 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 106 107 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 166 167 HGSDPSGRRITDSYCETWRTEAPAATGQASSLLAGRLIEQEAASCRHAFVVICIENSVWT 226 47 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 106 107 VRRADRIGVPVVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 166 61 VRRADRAAVPIVNLKDELLFPSWEALFSGSEGPLKPGARIFSFDGKDVLRHPTWPQKSVW 120 167 HGSDPSGRRITDSYCETWRTEAPAATGQASSILAGRLIEQEAASCRHAFVVICIENSVMT 226 121 HGSDPNGRRLTESYCETWRTEAPSATGQASSLLGGRLLGGSAASCHHAYIVLCIENSFWT 180 0; Gaps US-09-315-689-3
Sequence 3, Application US/09315689
Fatent No. 6346510
GENERAL INFORMATION:
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0229
CURRENT APPLICATION UNMER: US/09/315,689
CURRENT PILING DAFE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0 0; Gaps OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC // OTHER INFORMATION: PEPTIDE US-09-561-108-14 Query Match 67.4%; Score 835; DB 4; Length 182; Best Local Similarity 85.1%; Pred. No. 4.1e-86; Matches 154; Conservative 14; Mismatches 13; Indel8 Query Match 67.4%; Score 835; DB 4; Length 182; Best Local Similarity 85.1%; Pred. No. 4.1e-86; Matches 154; Conservative 14; Mismatches 13; Indels TYPE: PRT ORGANISM: Artificial Sequence PRIOR FILING DATE: 1999-04-2 NUMBER OF SEQ ID NOS: 44 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 14 TYPE: PRT ORGANISM: Homo sapiens 227 8 227 181 A 181 182 LENGTH: 182 US-09-315-689-3 SEQ ID NO 3 g ò g d g $\overset{\diamond}{\circ}$ 8 D. ò 8 ò ద ò

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US-09-561-526-14

| Sequence 14, Application US/09561526
| Sequence 14, Application US/09561526
| Sequence 14, Application US/09561526
| GENERAL INFORMATION:
| APPLICANT: Philip E. Thorpe
| APPLICANT: Rolf A. Brekken
| TITLE OF INVENTION: ANTHODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
| TILE OF INVENTION: ANTHODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
| CURRENT FILING DATE: 4001.002586
| CURRENT FILING DATE: 2000-04.28
| WINDER OF SEQ ID NOS: 44
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 14
| SEQ ID NO 14
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/ Sequence 14, Application US/09561499

/ Sequence 14, Application US/09561499

/ Patent No. 6524683

/ GENERAL INFORMATION:

/ APPLICANT: Philip B. Thorpe

/ APPLICANT: Rolf A. Brekken

/ TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF

/ TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF

/ TITLE OF INVENTION ON UNMERR: 4000-04-28

/ CURRENT FILING DATE: 2000-04-28

/ WUMBER OF SEQ ID NOS: 44

/ SOFTWARE: Patentin Ver. 2.0

/ SEQ ID NO 14
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-561-499-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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ORGANISM: Artificial Sequence
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47 HTHODFOLVLHLVALNSPOPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 106
                                                                                                166
                                                                                                                      167 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 226
                                                                                                                                                                                                                    121 HGSDPNGRRITESYCETWRTEAPSATGQASSLLGGRLLGQSAASCHHAYIVLCIENSFMT 180
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Patent No. 6201104

GENERAL INFORMATION:
APPLICANT: MacDonald, Nicholas
APPLICANT: Sim, Kim Lee
TITLE OF INVENTION: Anglogenesis-Inhibiting Protein Binding Peptides and
TITLE OF INVENTION: Proteins and Methods of Use
PILE REFERENCE: 05213-0370
                                           1 HSHRDFOPVLHLVALNSPLSGGMRGIRGADFOCFQQARAVGLAGTFRAFLSSRLQDLYSI
                                                                                           107 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVW
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APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
TITLE OF INVENTION: INHIBITING VEGF
FILE REFERENCE: 4001.00284.831
CURRENT APPLICATION NUMBER: US/09/998,831
CURRENT APPLICATION NUMBER: 09/551,108
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.4%; Score 835; DB 4; Length 182;
85.1%; Pred. No. 4.1e-86;
tive 14; Mismatches 13; Indels
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Patent No. 6676941
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ORGANISM: Artificial Sequence
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SOFTWARRE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 182
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Matches 154; Conservative
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US-09-998-831-14
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                                                                                                       47 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFQQARAAGLAGTFRAFLSSRLODLYSI 106
                                                                                                                                                                                                                     107 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 166
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                                                                                                                                           | SHRDFQPVLHLVALNSPLSGGMRGIRGADFQCPQQARAVGLAGTFRAFLSSRLQDLYSI
                                                     0; Gaps
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Sequence 5, Application US/09315689

Sequence 5, Application US/09315689

Sequence 5, Application US/09315689

Sequence 5, Application General Compositions

APPLICANT: OF TREATION: Application Compositions

TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions

FILE REFERENCE: 05213-0229

CURRENT APPLICATION NUMBER: US/09/315,689

CURRENT FILING DATE: 1999-05-20

NUMBER OF SEQ ID NGS: 6

SOFTWARE: Patentin Ver. 2.0
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Query Match 67.4%; Score 835; DB 3; Length 18: Best Local Similarity 87.4; Pred. No. 4.2e-86. Matches Batches 154; Conservative 14; Mismatches 13; Indels
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Patent No. 6080728
GENERAL INFORMATION:
APPLICANT: Mixson, James A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.9%
Matches 152; Conservative
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US-09-315-689-5
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US-08-985-526-36
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CURRENT APPLICATION NUMBER: US/09/206,059
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2

TYPE: PRT ORGANISM: Homo sapiens

US-09-206-059-2

183

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Mon Mar 29 17:32:19 2004
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118-09-938-391-2.ra

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Query Match 63.8%; Score 790; DB 3; Length 185; Best Local Similarity 81.1%; Pred. No. Se-81; Matches 150; Conservative 16; Mismatches 17; Indels
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107 VRRADRIGVPVV-NLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSV 165 166 WHGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVM 225 d

47 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 106

Gaps 7 2 HTHQDFQPVLHLVALNTPLSGGMRGIRGADFQCFNNAR-VGLSGTFRAFLSSRLQDLYSI 60

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181 TSFSR 185

Search completed: March 26, 2004, 13:39:22 Job time : 20.3333 secs

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Sequence 3010, Ap
Sequence 16, App
Sequence 3, Appli
Sequence 5, Appli
Sequence 49, Appli
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 56, Appl
Sequence 56, Appl
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Sequence 57, Appl
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1239
1 PWRADDILAGPPRLLDPQPY......CRHAFVVLCIENSVMTSFSK 230
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| cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB_pep:*
| cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB_pep:*
| cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*
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| cgn2_6/prodata/2/pubpaa/USO8_NEW_PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-264-049-3010
US-10-060-036-166
US-10-431-642-3
US-09-961-403-5
I US-09-938-391-4
I US-10-292-418-35
US-09-998-831-13
US-09-998-831-13
US-10-131-241-55
US-10-131-241-54
US-10-131-241-54
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US-10-042-347-34
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                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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a 32,	8-10-132-134-		3		88	43
e 4137	-10-425-114-4137		21	•	89	42
equence 4285	-10-425-114-42		m		89.5	41
e 8477,	0-156-761-8477		6239	٠	16	40
m '	-10-108-260A-37		43		91	39
ď.	-766-412-32		16		97	38
Sequence 1309	0-156-761-1	14	739	•	•	37
9, App	-10-308-644-	15	24		103	36
	10-016-569A-	5	24		0	35
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equence 1,	9-822-540A-	σ	63	4.	0	33
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equence 1	-10-292-4	14	æ	ė.	S	24
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equence 3	-10-080-79	13	0	7	3	22
equence 4	-10-131-241-	14	α	7	m	21
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equence 4	-10-292-41	14	α	7	m	19
in a	-10-131-24	14	ω	67.4	m	18
equence 1	10-080-797-1	13	ω	67.4	835	17
	09-873-676	თ	183	67.4	m	16

ALIGNMENTS

SULT 1 -09-938-391-3	OY 1 PWRADDILAGPPRILDPQPYPGAPHHGSYVHFQPARFTGGVWTHTHQDFQLVLHUVA 	QY 61 LNSPQPGGNRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNL 	OY 121 RDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDYLQHPAWFRKSVWHGSDPSGRRITDSY	Oy 181 CETWRIEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVWISFSK 230 Db 181 CETWRIEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVWISFSK 230
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1292 PWRADDILASPPRLPEPQPYPGAPHHSSYVHLRPARPISPP----AHSHRDFQPVLHLVA 1347
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                                                                                                                                                                                                                                                                                                                 61 LNSFQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVVU 120
                                                                                                                                                                                                                                                                                                                                                                                                                     121 RDBVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY 180
                                                                                                                                                                                                          1 PWRADDILAGPPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVA 60
                                                                                                 Query Match 82.2%; Score 1019; DB 14; Length 1516;
Best Local Similarity 82.4%; Pred. No. 5.9e-95;
Matches 187; Conservative 16; Mismatches 20; Indels 4; Gaps
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapien
US-10-431-642-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-049-3010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.2%; Score 1019; DB 15; Length 682;
Best Local Similarity 82.4%; Pred. No. 2.1e-95;
Matches 187; Conservative 16; Mismatches 20; Indels 4; Gaps 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 PWRADDILASPPRLPBPQPYPGAPHHSSYVHLRPARPTSPP----AHSHRDPQPVLHLVA 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 RDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY 180
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APPLICANT: Ralos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Aclos, Michael J.
APPLICANT: Hepler, Milliam T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REPERRACE: 210121.566
CURRENT APPLICATION NUMBER: US/10/660,036
CURRENT APPLICATION NUMBER: US/10/660,036
CURRENT APPLICATION OF 4560
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 166
LENGTH: 1516
                                                                                        Sequence 3010, Application US/10264049
Sequence 3010, Application US/10264049
Publication No. US20040005579A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRENCE: PAL33P1
CURRENT PELICATION NUMBER: US/10/264,049
CURRENT PILING DATE: 2002-10-04
PRIOR FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DC 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Petentin Ver. 3.1
LENGTH: 682
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US-10-060-036-166
US-10-060-036-166

, Sequence 166, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
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NAME/KEY: MISC FEATURE
LOCATION: (20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                             RESULT 2
US-10-264-049-3010
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1348 INSPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSIVRRADRAAVFIVNL 1407
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Best Local Similarity 82.4%; Pred. No. 5.9e-95;
Matches 187; Conservative 16; Mismatches 20; Indels 4; Gaps
                                                                                                                                                                                                           Sequence 3, Application US/10431642;
Sequence 3, Application US/10431642;
Publication No. US20040009920A1
GENERAL INFORMATION:
APPLICANT: RUGBLART, Erkki
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
TITLE OF INVENTION: TUMOR GROWTH AND ANGIOGENESIS
FILE REPERENCE: BURNHAM.008CTP
CURRENT APPLICATION NUMBER: US/10/431,642
CURRENT FILING DATE: 2003-05-05
PRIOR PELLING DATE: 2001-12-03
PRIOR PILING DATE: 2001-12-03
PRIOR PILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASSEQ for Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
                                       1468 CETWRTEAPSATGQASSLLGGRLLGQSAASCHHAYIVLCIENSFWTA 1514
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181 CETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMTS 227
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) ORGANISM; Canine sp. US-10-131-241-49
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Bublication No. US20030158099A1

GENERAL INFORMATION.

APPLICANT: Tong, et al.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING

TITLE OF INVENTION: DISORDERS INVOLVING ANGIOGENESIS

FILE REFERENCE: PC10790A

CURRENT PAPLICANTON NUMBER: US/09/938,391

CURRENT FILING DATE: 2001-08-24

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 4

SEQ ID NO 4

SEQ ID NO 4
APPLICANT: KRAETZSCHMAR, DOENN; APPLICANT: KRAETZSCHMAR, DOENN; APPLICANT: KREFT, BERTHOLT; APPLICANT: WINTERHAGER, ELKE; APPLICANT: WINTERHAGER, ELKE; APPLICANT: SCOTTI, SIMONE; ITILE OP INVENTION: MATHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS; FILE REFERENCE: SCH-1789 CURRENT APPLICATION NUMBER: US/09/961,403; CURRENT FILING DATE: 2001-09-25; NUMBER OF SEQ ID NOS: 15
5 SOFTWARE: PATENTIN VOS: 15
5 SEQ ID NO 5
5 LENGTH: 684
7 TYPE: PPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.0%; Score 1003; DB 10; Length 684; 81.5%; Fred. No. 9.1e-94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 78.0%; Score 966; DB 10; Length 184; Best Local Similarity 100.0%; Pred. No. 1e-90; Matches 184; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 185; Conservative 15; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: CANINE ENDOSTATIN AMINO ACID SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Homo sapiens
US-09-961-403-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Best Local (
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RESULT 8
US-10-292-418-35
US-10-292-418-35
| Sequence 35, Application US/10292418
| Publication No. US20030139365A1
| GENERAL INFORMATION:
| APPLICANT: Lo, Kin-Ming
| APPLICANT: Lo, Kin-Ming
| APPLICANT: Lo, Kin-Ming
| APPLICANT: Lo, Kin-Ming
| APPLICANT: Lo, Kin-Ming
| APPLICANT: Lo, Kin-Ming
| APPLICANT: Lo, Kin-Ming
| APPLICANT: Lo, Content of Application and Export of Angiogenesis Inhibitors as
| TITLE OF INVENTION: Emmunofusins
| TITLE OF INVENTION: Immunofusins
| TITLE OF INVENTION: LEX-0061
| CURRENT FILING DATE: 2002-11-12
| PRIOR FILING DATE: 1999-08-25
| PRIOR FILING DATE: 1999-08-25
| PRIOR FILING DATE: 1998-08-25
| NUMBER OF SEQ ID NOS: 54
61 VRRADRIGVPVVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 HGSDPSGRRLIDSYCETWRTEAPAATGQASSLLAGRLLEGEAASCRHAFVVLCIENSVMT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQBAASCRHAFVVLCIENSVMT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                             47 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 106
                                                                                                                                                                                                                                                                                                                                                         107 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKFGARIFSFDGRDVLQHPAWPRKSVW 166
                                                                                                                                                                                                                                                                                                                                                                                          61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 HGSDPSGRRITDSYCETWRTEAPAATGQASSILLAGRLIEQEAASCRHAFVVILCIENSVMT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 HTHTHTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQD 102
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; Sequence 13, Application US/09998831
; Patent No. US20020119153A1
; GENERAL INPOMATION:
    APPLICANT: Philip E. Thorpe
; APPLICANT: Philip E. Thorpe
; TITLE OF INVENTION: ANTIBODY CONUGATE COMPOSITIONS FOR SELECTIVELY
TITLE OF INVENTION: INHIBITING VEGF
; TITLE OF INVENTION: UNMER: US/09/99,831
CURRENT PILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/561,108
; PRIOR FILING DATE: 2000-04-28
; WUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.0
; FROMTH.
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                                                                                                                                                              Query Match 77.4%; Score 959; DB 14; Length 184; Best Local Similarity 99.5%; Pred. No. 5.3e-90; Matches 183; Conservative 0; Mismatches 1; Indels C
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35
LENGTH: 184
                                                                     ; TYPE: PRT; ORGANISM: Canis familiaris US-10-292-418-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 SVMTSFSK 230
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APPLICANT: Holaday, John W.
APPLICANT: Holaday, John W.
APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliff
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REPERENCE: 05213-0344 41170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 1999-007-22
PRIOR PELING DATE: 1999-00-06
PRIOR FILING DATE: 1999-06-21
PRIOR FILING DATE: 1999-06-21
PRIOR PELING DATE: 1999-05-22
NUMBER OF FILING DATE: 1999-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATCH IN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 HTHTHTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLQD 102
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NS-10-373-561-13

// Sequence 13, Application US/10373561

// Sequence 13, Application US/10373561

// Sequence 13, Application Wo. US203017527641

// GENERAL INFORMATION:
// APPLICANT: Philip B. Thorpe
// APPLICANT: Rolf A. Brekken
// TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
// TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
// CURRENT APPLICATION NUMBER: US/10/373,561
// PRIOR PAPLICATION NUMBER: US/09/561,499
// PRIOR PELING DATE: 2000-04-28
// PRIOR PELING DATE: 1999-04-28
// NUMBER OF SEQ ID NOS: 44
// SOFTWARE PARENTING PARE: 42
// SEQ ID NO 13
// SEQ ID NO 13
// LENGTH: 191
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88.0%; Score 843; DB 14; Length 191;

Best Local Similarity 83.0%; Pred. No. 4.3e-78;

Matches 156; Conservative 17; Mismatches 15; Indels 0
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; Sequence 55, Application US/10131241
; Septencion No. US20030012792A1
; GENERAL INFORMATION:
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| Sequence 14, Application US/09998831
| Sequence 14, Application US/09998831
| GENERAL INFORMATION:
| APPLICANT: Philip E. Thorpe
| APPLICANT: Rolf A. Brekken
| TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
| TITLE OF INVENTION: INHIBITING VEGF
| FILE REFERENCE: 4001.002584
| CURRENT FAPLICATION NUMBER: US/09/998,831
| CURRENT FILING DATE: 2000-04-28
| PRIOR FILING DATE: 2000-04-28
| VINMER OF SEQ ID NOS: 44
| SOFTWARE: PATENTION OF: 24
| SOFTWARE: PATENTION OF: 2.0
| SEQ ID NO 14
| LENGTH: 182
| TYPE: PRT
| TYPE: PRT
| CRANTISM: Artificial Sequence
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                     13; Indels
Best Local Similarity 85.1%; Pred. No. 2.7e-77;
Matches 154; Conservative 14; Mismatches 13
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, Sequence 54, Application US/10131241
; Publication No. US20030012792A1
; GENERAL INFORMATION:
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Best Local Similarity 85.19
Matches 154; Conservative
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US-09-998-831-14
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RESULT 14
195-10-042-347-3
1 Sequence 3. Application US/10042347
2 Sequence 3. Application WS/10042347
2 Sequence 3. Application No. US20030114370A1
3 GENERAL INFORMATION:
3 APPLICANT: O'Reilly, Michael S.
4 APPLICANT: O'Reilly, Michael S.
5 TITLE OF INVENTION: Michael Acid Molecules Encoding Endostatin Protein and Peptide F.
7 TITLE OF INVENTION: Thereof (41170-249974)
5 TITLE OF INVENTION: Thereof (41170-249974)
5 TITLE OF INVENTION: WINGER: US 09/315,689
7 TITLE OF INVENTION: WINGER: US 09/315,689
7 FILE REPERBORE: 1999-05-20
7 FILING DATE: 1998-10-62
7 FILING DATE: 1998-10-16
7 FILING DATE: 1998-09-16
7 FILING DATE: 1998-09-16
7 FILING DATE: 1996-09-16
7 FILING DATE: 1996-09-23
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7 FILING DATE: 1996-09-17
7 FILING DATE: 1996-09-17
7 FILING DATE: 1996-09-17
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolife
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REPERENCE: 05219-034 4 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-05-22
NUMBER OF SEQ ID NOS: 65
ROUTH APPLICATION NUMBER: US 60/086,586
PRIOR PLING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
SOFTHWARE: PATCHTIN VERSION 3.1
SEQ ID NO 54
LENGTH: 182
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ORGANISM: Homo sapiens
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US-10-131-241-54
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181 A 181
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107 VRRADRIGVPVVVLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 166
                                                                                                                                                                                                                       61 VRRADRAAVDIVNLKDELLFPSWEALFSGSEGPLKFGARIFSFDGKDVLRHPTWPQKSVW 120
                                                                                                                                                                                                                                                                                                                   61 VRRADRAAVPIVNLKDELLFPSWEALFSGSEGPLKFGARIFSFDGKDVLRHPTWPQKSVW 120
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                                                                                                                                     1 HSHRDFQPVLHLVALNSPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/10373561
; Sequence 14, Application US/10373561
; Publication No. US20030175276A1
; Publication No. US20030175276A1
; GABERAL INFORMATION:
   APPLICANT: Philip B. Thorpe
   APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTHEOPY METHODS FOR SELECTIVELY INHIBITING VEGF
FILE REPERSICE: 4001.002582
; CURRENT APPLICATION NUMBER: US/10/373,561
; CURRENT APPLICATION NUMBER: US/20/561,499
; PRIOR FILING DATE: 2003-02-4
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; SEQ ID NO 14
                                                                                           47 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLODLYSI
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                                               0; Gaps
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US-10-373-561-14
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Query Match 67.4%; Score 835; DB 14; Length 182; Best Local Similarity 85.1%; Pred. No. 2.7e-77; Matches 154; Conservative 14; Mismatches 13; Indels
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ORGANISM: Artificial Sequence
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

March 26, 2004, 13:33:07; Search time 15.5556 Seconds (without alignments) 1422.260 Million cell updates/sec Run on:

US-09-938-391-2 1239 1 PWRADDILAGPFRLLDPQPY......CRHAFVVLCIENSVMTSFSK 230 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	collagen alpha 1(X	collagen alpha 1(X	collagen alpha 1(X	collagen alpha 1(X	hypothetical prote	sulfolipid biosynt	58K membrane-assoc	w	hypothetical prote			ataxin-1 - human	alginate biosynthe	hypothetical prote	hypothetical prote	NAD(P)-arginine AD	hypothetical prote	protein-tyrosine k	HC-toxin synthetas	hypothetical prote	DNA-binding protei	RhoGAP protein hom	polyketide synthas	probable transcrip	NAD(P)-arginine AD	probable transfera	Vgr prot	vgr proc	probable phospholi
SUMMARIES	OI	A53019	B56101	A56101	A53317	T22002	C45729	A53798	T44743	G90781	D85642	T34086	S46268	A83204	T36945	G75295	A55461	T17336	TVHUY2	A45086	T20387	A41537	H59432	T30283	T36950	B55461	T34842	~	ഹ	ம
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PQ0054	AC2276	B83386	T45096	G83127	D90658	D85509	T30418	T36083	T49804	138547	T42045	C87288	AG2726	C97508	S52622	
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80.5	80	80	80	79.5	79.5	79.5	7	7	7.9	78.5	78.5	78	78	78	78	
30	31	32	33	3.4	35	36	37	38	68	40	41	42	43	44	4.5	

ALIGNMENTS

RESULT 1 A53019

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A,Gross-references: MGI.71175
A,Map position: 10:41.0
A,Gross-references: MGI.71175
A,Map position: 10:41.0
A,Introns: 1295/3; 1310/1; 1331/1; 1345/3; 1388/3; 1437/1; 1461/3; 1505/3; 1516/3; 1595
A,Mote: the list of introns is incomplete
C,Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteogly
C,Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteogly
C,Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteogly
C,Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteogly
C,Keywords: alternative splicing; angiogenesis inhibitor; doma splice form #status predicted <COO1>
F; 1-239,487-1774/Product: collagenous #status predicted <COO2>
F; 86 812/Domain: collagenous #status predicted <COO6>
F; 106-1146/Domain: collagenous #status predicted <COO6>
F; 106-1146/Domain: collagenous #status predicted <COO6>
F; 107-1333/Region: collagenous #status predicted <COO6>
F; 1351-1333/Region: collagenous #status predicted <COO6>
F; 1351-1333/Region: collagenous #status predicted <COO6>
F; 1442-1449/Domain: c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 ALNSPOPGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLODLYSIVRRADRIGVPVVN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PWRADDILAGPPRLLDPQPYPGAP-HHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1724 YCETWRIETTGAIGQASSLISGRLIEQKAASCHNSYIVLCIENSFMTSFSK 1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 YCETWRIEAPAAIGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMISFSK 230
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Best Local Similarity 80.1%; Pred. No. 1.9e-81;
Matches 185; Conservative 18; Mismatches 23; Indels
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A; Residues: 487-1146, 'L', 1148-1193, 'F', 1195-1210, 'R', 1212-1512, 'L', 1514-1522, 'F', 1524-16
A; Residues: 487-1146, 'L', 1148-1193, 'F', 1195-1210, 'R', 1212-1512, 'L', 1514-1522, 'F', 1524-16
A; Cross-references: EMBL:122545, NID:9348968; PIDN:AAA19767.1; PID:9511298
B; Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 4229-4233, 1994
A; Title: Isolation and sequencing of cDNAs for proteins with multiple domains of Gly-Xaa
A; Reference number: A58370; MUD:94240111; PMID:8183893
A; Molecule type: mRNA
A; Residues: 487-1512, 'L', 1514-1522, 'F', 1524-1683, 'V', 1685-1774 < OH2>
A; Cross-references: EMBL:122545
B; A; A; Muragaki, Y.; Yoshioka, H.; Inoue, H.; Ninomiya, Y.
Biochem: Biophys. Res. Commun. 196, 576-582, 1993
A; Title: Identification of a novel collagen chain represented by extensive interruptions
A; Reference number: PNO675; MUD:94059075; PMID:8240330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ם
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collagen alpha 1(XVIII) chain precursor, long splice form - mouse

NyContains: collagen alpha 1(XVIII)

NyContains: collagen alpha I(XVIII)

C)Species: Mus musculus (house mouse)

C)Species: Mus musculus (house mouse)

C)Date: 03-0ct-1995 #sequence revision 08-May-1998 #text change 15-Sep-2003

C)Date: 03-0ct-1995 #sequence revision 08-May-1998 #text change 15-Sep-2003

C)Date: 03-0ct-1995 #sequence revision 08-May-1998 #text change 15-Sep-2003

R)Rehn, M.; Pihlajaniemi, T.

J. Biol. Chem. 270, 4705-4711, 1995

A)Title: Identification of three N-terminal ends of type XVIII collagen chains and tissu tif homologous to rat and Drosophila frizzled proteins.

A)Reference number: A56101; MUID:95181468; PMID:7876242
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A; Residues: 1591-1610 < ORE>
A; Residues: 1591-1610 < ORE>
A; Residues: 1591-1610 < ORE>
A; Note: inhibits endothelial cell proliferation
C; Comment: Prolines and Veines at the third position of the tripeptide repeating unit lated and subsequently O-glycosylated
C; Comment: The different splice forms of collagen alpha 1(XVIII) may be involved in per C; Comment: The different splice forms of collagen alpha 1(XVIII) may be involved in per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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A; Molecule type: DNA; mRNA
A; Residues: 1293-1403, '1405-1774 <REH3>
A; Residues: 1293-1403, '1405-1774 <REH3>
A; Cross-references: GB: U03/14; NID:9487733; PIDN:AA20657.1; PID:9487734
A; Cross-references: GB: U03/14; NID:9487733; PIDN:AA20657.1; PID:9487734
A; Cross-references: GB: U03/14; NID:948773; PIVIN, IC 18 B; Z77-285, 1997
A; Title: Endostatin: an endogenous inhibitor of angiogenesis and tumor growth.
A; Reference number: A58816; MUID:97160848; PMID:9008168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-239,487-562 <REH2>
A;Cross-references: CB:Ull637; NID:g618429
A;Experimental source: splice form clones PEB.1, PEI9, PEI5.2
A;Experimental source: splice form clones PEB.1, PEI9, PEI5.2
R;Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, B.R. submitted to the EMBL Data Library, August 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A,Readdudes: 1-562 <REM1).
A):Cross-references: GB:U11637; NID:g618429; PIDN:AAC52179.1; PID:g618430
A):Experimental source: splice form clone PE17.24
181 CETWRIBAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMTS 227
                                                        636 CETWRTEAPSATGQASSLLGGRILGQSAASCHHAYIVLCIENSFMTA 682
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A; Residues: 635-1774 <ABE>
R; Rehn, M.; Hintikka, E.; Pihlajaniemi, T.
J. Biol. Chem. 269, 13929-13935, 1994
A; Tile: Primary structure of the alphal chain of mouse collagen chain.
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A;Accession: S72450
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DB 2; Length 1774;

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from collagen alpha 1(XVIII) chain by

C;Comment: Endostatin is released from ay be useful in treating solid tumors.

635

576

ACOUTAINS: endostatin
Collage alpha 1(XVIII) chain precursor, short splice form - mouse
Nocontains: endostatin
C;Species: Mus musculus (house mouse)
C;Accession: Asequence revision 08-May-1998 #text_change 15-Sep-2003
C;Accession: As6101; As8371; S72450; S65595
R;Rehn, M.; Pihlajaniemi, T.
C;Accession: As6101; Anos-711, 1995
A;Title: Identification of three N-terminal ends of type XVIII collagen chains and tist
Lif homologous to rat and brosophila frizzled proteins.
A;Reference mumber: As6101; MUID:95181468; PMID:787642
A;Accession: As6101
A;Molecule type: mRNA
A;References: GB:U11636; NID:g618427; PIDN:AAC52178.1; PID:g618428
A;Reshn, M.; Pihlajaniemi, T.
Proc. Natl. Acad. S61: U.S.A. 91, 4234-4238, 1994
A;Reference number: As6371; MUID:94240112; PMID:8183894
A;Reference number: As8371; MUID:94240112; PMID:8183894
A;Residues: 1-928 <RRHz>

RESULT 5 g 8 셤 ò 원 ò 8 A;Accession: S72450
A;Molecule type: mRNA
A;Residue type: mRNA
A;Residue type: mRNA
A;Residue type: mRNA
A;Cross-references: 28-687, 'L', 689-734,'F',736-751,'R',753-1315 <OHW>
A;Cross-references: 28-687, 'L', 689-734,'F',736-751,'R', 753-1315 <OHW>
A;Cross-references: 28-687, 'L', 689-734,'F', Timmons, S.; Ooshima, A.; Olsen, A.B.R.
B;Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 4229-4233, 1994.
A;Title: Isolation and sequencing of CDNAs for proteins with multiple domains of Gly-Xas
A;Reference number: A58370; MUID:94240111; PMID:8183893 A, Molecule type: mRNA A, Residues: 28-1315 COHS> A; Residues: 28-1315 COHS> C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit (lated and subsequently O-glycosylated C; Comment: The different splice forms of collagen alpha 1(XVIII) may be involved in peri C; Comment: Endostatin is released from collagen alpha 1(XVIII) chain by the action of un 1089 PWRADDILANPPRIPDROPYPGVPHHHSSYVHLPPARPT----LSLAHTHQDFQPVLHLV 1144 1264 179 60 ALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRIGVPVVN 119 A;Cross-references: GB:L16898; NID:g404754; PIDN:AAA37434.1; PID:g553894 R;Oh, S.P.; Kanagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, B.R. submitted to the EMBL Data Library, August 1993 A;Reference number: S72450 1 PWRADDILAGPPRILIDPQPYPGAP-HHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLV 120 IRDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLOHPAWPRKSVWHGSDPSGRRLTDS 1265 YCETWRIETTGAIGQASSLLSGRLLEQKAASCHNSYIVLCIENSFMISFSK 1315 180 YCETWRTEAPAATGQASSILAGRILEQEAASCRHAFVVLCIENSVMTSFSK 230 5; 79.1%; Score 980.5; DB 2; Length 1315; 79.7%; Pred. No. 2.5e-81; tive 19; Mismatches 23; Indels 5; A53317 collagen alpha 1(XV) chain precursor - human N,Alternate names: procollagen alpha 1(XV) chain C;Species: Homo sapiens (man) ay be useful in treating solid tumors. C;Genetics: A;Gene: MGI:Coll8al Query Match Best Local Similarity 79.7% Matches 184, Conservative A;Cross-references: MGI:71175 A;Map position: 10:41.0 원 임 셤 à ò ઠે

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C;Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text_change 15-Sep-2003
C;Accession: A53317; A53146; S28778
R;Kivirikko, S.; Heinaemaeki, P.; Rehn, M.; Honkanen, N.; Myers, J.C.; Pihlajaniemi, T. J. Biol. Chem. 269, 4773-4479; 1994
A;Tile: Primary structure of the alphal chain of human type XV collagen and exon-intro A;Reference number: A53317; MUID:94148920; PMID:8106446
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submitted to the EMBL Data Library, October 1996
A;Reference number: Z19500
A;Accession: T22002
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-650 <WIL>
A;Coss-references: EMBL: Z81079; PIDN: CAB03084.1; GSPDB:GN00019; CESP: F39H11.4
A;Experimental source: clone F39H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 GIRGADFOCFQQARAAGLAGTFRAFLSSRLODLYSIVRRADRIGVPVVNLRDEVLFPSWE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 ALFSGSBGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSYCETWRTBAPA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T22002
hypothetical protein F39H11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 PPRLLDPQPYPGAPHHGSYVHFQPARPIGGPVHTHTHTHQDFQLVLHLVALNSPQPGGMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Genera GDS: COLLINE GDS: 132578; OMIN: 120325
A,Cross-references GDS: 132578; OMIN: 120325
A,Map position: 9q21-9q2
F;1-22/Domain: signal sequence #status predicted <SIG>
F;1-22/Domain: signal sequence #status predicted <MAT>
F;23-1388/Product: collagen alpha 1(XV) chain #status predicted <MAT>
F;1216-1388/Region: multiplexin collagen carboxyl-terminal homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 48.2%; Pred. No. 5.8e-40;
Matches 106; Conservative 30; Mismatches 63; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 ATGOASSILAGRILEQEAASCRHAFVVLCIENSVMTSFSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Status: preliminary
A,Molecule type: mRNA
A,Molecule type: mRNA
C,Genetics:
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RiJuang, S.H.; Huang, J.; Li, Y.; Salas, P.J.I.; Fregien, N.; Carraway, C.A.C.; Carrawa J. Biol. Chem. 269, 15067-15075, 1994
A; Title: Molecular cloning and sequencing of a 58-kDa membrane- and microfilament-assoc A; Reference number: A53798, MUID:94253065; PMID:8195143
A; Accession: A53798
A; Accession: A53798
A; Accession: A53798
A; Residues: preliminary, not compared with conceptual translation
A; Residues: L427 cJUA>
A; Residues: L427 cJUA>
C; Superfamily: mammalian retrovirus gag polyprotein I
C; Keywords: actin binding; monomer; phosphoprotein
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C,Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 QPGGMRGIR----GADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRR---ADRTGVPV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 VNLRDEVLF---PSW------EALFSGSEGQ---LKPGARIFSFDGRDVLQ----HPAW 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 INSPORGOMEGIRGADFOCFOOARAAGLAGTFRAFLSSRLODLYSIVRRADRIGVPVVNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 DLLLEEPP----PYPVPTAPPREEEVE-PPARP---------RLEAAPSP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 GLPPRPGVIRD-RGTQ---LQRARAGEITAEM-AFI-------ADREGMPAELV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 PYPGAPHHGSYVHFQPARPIGGP-----VHTHTHIQDF------QLVLHLVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 PIPGS----SKAYREVANPDGGPSLRVPFRRVHLSTGAHFDLYDTSGPYTDPDAVINLTA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable thiamin biosythesis protein thiC [imported] - Mycobacterium lepraee (2,5pecies Mycobacterium lepraee (2,5pecies Nycobacterium lepraee (2,5pecies 1-Jan-2000 #text_change 18-Feb-2000 (2,Accession: T44743 This T44743 This T44743 This T44743 This Taylones (2,5pacies Taylones (2,5p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 P-RKSVWHGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 PLTRPDWDFTTAEGRRHURLYRQLLLAGLRGAARRPTNLAQVKQVVQEAAETPSAFL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 DDILAGPPRILLDPOPYPGAPHHGSYVHFOPARPTGGPVHTHTHTHQDFQLVLHLVALNSP
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Best Local Similarity 27.4%; Pred. No. 1.1;
Matches 43; Conservative 14; Mismatches 49; Indels 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.9%; Score 98; DB 2; Length 427; 24.9%; Pred. No. 0.32; tive 29; Mismatches 97; Indels
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-547 <JAM>
A,Residues: 1-547 <JAM>
A,Experimens: EMBL:AL035159; PIDN:CAA22712.1
A,Experimental source: cosmid B1450
C,Genetics:
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Best Local Similarity
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C;Species: Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Accesion: C45729; 827664
R;Benning; C; Somerville, C: Somerville, C: Somerville, C: Somerville, C: Somerville, C: A: A: Title: Identification of an operon involved in sulfolipid biosynthesis in Rhodobacter A;Reference number: A45729; MUID:93015699; PMID:1400200
A;Status: preliminary
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                             93 RAFLSSRLQDLYSIVRRADRTGVPVVVVLRDEVLFPSWEALFSGSEGQLXPGARIFSFDGR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          502 RAMLSSNVQDLVRIVHSVD-FDTTVVNVAGHHLFPSWRSFVNGA--QMNPHAKLFSFDRH 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 DVLQHPAWPRKSVWHGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAAS-- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 SGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSYCETWR----- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 GADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNLRDEVLFPSWEALF 133
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                                                                                                                                                                                                                                                                                                                                                                                          33 QPARPTGGPVHTHTHTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTF 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 LLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVALNSPQPGGMRGIR 73
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NyAlternate names: 58K microfilament-associated protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-00c1-1994 #sequence_revision 07-0ct-1994 #text_change 24-Nov-1999
C;Accession: A53798
                                                                                                                                                                                                               Query Match 29.8%; Score 369.5; DB 2; Length 650; Best Local Similarity 41.7%; Pred. No. 8e-26; Matches 80; Conservative 27; Mismatches 70; Indels 15; Gaps
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8.0%; Score 99; DB 2; Length 244;
Best Local Similarity 23.9%; Pred. No. 0.13;
Matches 56; Conservative 28; Mismatches 96; Indels 54; Gaps
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C;Genetics:
A;Gene: sqdC
A;Start codon: GTG
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                                                                                   A;Map position: 1
A;Introns: 109/3; 154/1; 357/1; 420/3; 464/3; 566/2; 594/1; 628/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 CRHAFWALCIEN 222
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A; Residues: 1-244 <BEN>
                                              Gene: CESP:F39H11.4
         Genetics:
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111 DRTGVPVVNIRDEVIFPSWEALFSGSEGQLKPGARIESFDGR	Apportmentical protein Cobs. 4 - Caenormaballis elegams C.Species: Caenorhabditis elegans C.Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C.Accession: T34086 R.Le, T. Submitted to the EMBL Data Library, November 1995 A.Description: The sequence of C. elegans cosmid C0687. A.Reference number: 221474 A.Accession: T34086 A.Status: preliminary; translated from GB/EMBL/DDBJ	A, Molecule type: DNA A, Molecule type: DNA A, Residues: 1-335 <let> A, Fessidues: 1-335 <let> A, Cross-references: EMBL: U41009; PIDN: AAA82281.1; CESP: CO6E7.4 C, Genetics: CESP: CO6E7.4 A, Gene: CESP: CO6E7.4 A, Introns: 41/2; 83/1; 116/3; 219/1; 273/3</let></let>	Query Match Query Match Query Matches 20; Conservative 4; Mismatches 22; Indels 20; Gaps 3; Matches 20; Conservative 4; Mismatches 22; Indels 20; Gaps 3; Qy PWRADDILAGPPRILDPQPYPGAPHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVA 60	Oy 61 LNSPOP 66	C;Genetics: A;Gene GDB:SCAL A;Gene: GDB:
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: G90781 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: G90781 A;Residues: 1-404 cHAx> A;Cross-references: GB:BA000007; PIDN:BAB34646.1; PID:g13360683; GSPDB:GN00154 A;Residues: 1-404 cHAx> A;Cross-references: GB:BA000007; PIDN:BAB34646.1; PID:g13360683; GSPDB:GN00154 A;Gene: EC51223	Query Match Best Local Similarity 25.5%; Pred. No. 1.6; Matches 73; Conservative 28; Mismatches 107; Indels 78; Gaps 18; Qy 9 AGPPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHL 58	113 VDAĞRMSQQRTKPNLASSARTLLĞTYFNDLQDQCAIVHLAGARGDFVA 1 111 DRTGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGR 1 112 DRTILPTAEHPEFKKIMINDVLPPTHDRHFFGGDATSFEQIE-AADIFSIGLVDNLSLFI 2	Qy 153 DVLQHPAWPRKSVWHGSDPSGRLTDSYCETWRTEAPATGQASSLL 199	RESULT 10 D85642 hypothetical protein Z1479 [imported] - Escherichia coli (strain O157:H7, substrain EDL9 C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: D85642 R;Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, Li: Gronbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, S29-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Scatus: preliminary A;Residues: DAA A;Residues: 1-404 cSTO> A;Cross-references: GB:AE005174; NID:g12514332; PIDN:AAG55600.1; GSPDB:GN00145; UWGF:Z14 C;Genetics: A;Gene: Z1479	Query Match Best Local Similarity 25.5%; Fred. No. 1.6; Matches 73; Conservative 28; Mismatches 107; Indels 78; Gaps 18; Qy 9 AGPPRLLDPQPYFGAPHHGSYVHFQPARFTGGPVHTHTTHQDFQLVLHL 58

A;Cross-references: EMBL:AL109962; PIDN:CAB53130.1; GSPDB:GN00070; SCOEDB:SCJ1 A;Experimental source: strain A3(2) C;Genetics: A;Gene: SCOEDB:SCJ1.12	Query Match 6.9%; Score 85.5; DB 2; Length 508; Best Local Similarity 22.6%; Pred. No. 5.6; Matches 60; Conservative 30; Mismatches 100; Indels 75; Gaps	QY 4 ADDILAGPPRLLDPQPYPGAPHGSYVHFQPARPTG QY 4 ADDILAGPPRLLDPQPYPGAPHHGSYVHFQPARPTG DD 204 ADDVFCLGDGPRILDCLEFDDALRYVDGLDDAAFLAMDLESLGAPESAAFFLAQYGBYSG	Qy 40 GPVHTHTHTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAA Db 264 DPAPPSLWHHYVAYRAFVRAKVSLIQARQGAPGAHATARRLVRMALRHLRASAVGLTLVA	ain PA J.; Br ; Lim, patho	r.; rac	A;Cross-references: GB:AB002058; GB:AE000513; NID:g6460059; PIDN:AAF11808.1 A;Experimental source: strain R1 C;Genetics: A;Gene: DR225 A;Map position: 1 Query Match Best Local Similarity 22.1%; Pred. No. 3.2; Matches 54; Conservative 17; Mismatches 87; Indels 86; Gaps	HFQPARPIGGPVHTHTHTHQDFQLVLF 	Qy 67 G
60 ALNSPQPGGWR-GIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRAD 111	112 RIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAMPRKSVWHGS 169	170 DPSGRRLT	216 V 216 435 I 435	AB3104 13 A83204 alginate blosynthesis protein Alg8 PA3541 [imported] - Pseudomonas aeruginosa (str. CiSpecies: Pseudomonas aeruginosa ciSpecies: Pseudomonas aeruginosa (str. CiSpecies: Pseudomonas aeruginosa ciSpecies: Pseudomonas aeruginosa (str. CiSpecies: Pseudomonas aeruginosa AB3204 Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M., Antire: 406, 959-964, 2000 M.V. Nature 406, 959-964, 2000 M.V. Nature 406, 959-964, 2000 A.A.; Earbig, K. A.; Larbig, K. A.; A.; Comper Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A, Reference number: A82950; MUID:20437337; PMID:10984043 A, Residues: DNA A, Residues: 1-494 <sto. 1-494="" 1-604="" <sto.="" a,="" c,="" genetios:<="" residues:="" seco.="" td=""><td>Query Match Query Match Query Match Rest Local Similarity 24.6%; Pred. No. 3.9; Best Local Similarity 24.6%; Pred. No. 3.9; Matches 45; Conservative 20; Mismatches 68; Indels 50; Gaps 7; So ODPQLVIHIVALNSPQPGMRGIRGADFQCFQQARAAGLAGTFRAFLSSR 99; </td><td></td><td>150 YCE 182 219 PCE 221</td><td>RESULT 14 T36945 Hypothetical protein SCJ1.12 - Streptomyces coelicolor Clyperies: Streptomyces coelicolor Clyperies: Streptomyces coelicolor Clyperies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 Clyccession: T36945 Clyperies: 04-Dec-1999 #sequence_revision N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, September 1999 Algebrance number: Z21607 Algebrance number: Z21607 Algebrance preliminary; translated from GB/EMBL/DDBJ Algebrance preliminary; translated from GB/EMBL/DDBJ</td></sto.>	Query Match Query Match Query Match Rest Local Similarity 24.6%; Pred. No. 3.9; Best Local Similarity 24.6%; Pred. No. 3.9; Matches 45; Conservative 20; Mismatches 68; Indels 50; Gaps 7; So ODPQLVIHIVALNSPQPGMRGIRGADFQCFQQARAAGLAGTFRAFLSSR 99;		150 YCE 182 219 PCE 221	RESULT 14 T36945 Hypothetical protein SCJ1.12 - Streptomyces coelicolor Clyperies: Streptomyces coelicolor Clyperies: Streptomyces coelicolor Clyperies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 Clyccession: T36945 Clyperies: 04-Dec-1999 #sequence_revision N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, September 1999 Algebrance number: Z21607 Algebrance number: Z21607 Algebrance preliminary; translated from GB/EMBL/DDBJ Algebrance preliminary; translated from GB/EMBL/DDBJ

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Search completed: March 26, 2004, 13:38:38 Job time : 19.5556 secs

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OM protein - protein search, using sw model	March 26, 2004, 13:29:16; Search time 11.6667 Seconds (Without alignments) 1026.526 Million cell updates/sec
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US-09-938-391-2 1239 1 PWRADDILAGPPRLLDPQPY......CRHAFVVLCIENSVMTSF8K 230 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues

141681 Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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WEDLINE-10000145; PubMed-1094434,

WEDLINE-10000145; PubMed-1094434,

Collegen W.YIII, Containing an endogenous inhibitor of angiogenesis and tumor growth, plays a critical role in the maintenance of retinal man would be compared to the collegen with the maintenance of retinal man would be collegen with the collegen
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Probom, PD000007; Clg_helix; 1.

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RARET; SN00281; TSPN; 1.

RARECILLULAR matrix; Connective tissue; Repeat; Hydroxylation; Call adhesion; Collagen; Glycoprotein; Signal; Alternative splicing; Polymorphism; 3D-structure. POTENTIAL.

RIGNAL 1 23 COLLAGEN ALPHA 1(XVIII) CHAIN.

RIGNAL 221 409 TERNITAL.

TOMAIN 134 1516 ENDOSTATIN.

TOMAIN 221 409 TERPLE-HELICAL REGION 1 (COLI).

TOMAIN 551 560 NONHELICAL REGION 1 (COLI).

TOMAIN 551 560 NONHELICAL REGION 2 (COL2).

TOMAIN 551 640 TRIPLE-HELICAL REGION 3 (COL2).

TOMAIN 665 786 TRIPLE-HELICAL REGION 3 (COL2).

TOMAIN 787 809 TRIPLE-HELICAL REGION 4 (COL4).

TOMAIN 893 906 NONHELICAL REGION 5 (COL5).

TOMAIN 994 961 TRIPLE-HELICAL REGION 5 (COL5).

TOMAIN 949 961 NONHELICAL REGION 6 (COL5).

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TOMAIN 961 MONHELICAL REGION 6 (COL5).

TOMAIN 962 1034 MINDHELICAL REGION 6 (COL6).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GALNAC. .) (POTENTIAL).
FT10a-CAR_000150.
BY SIMILARITY.
EY SIMILARITY.
CELL ATTACHGRITY SITE (POTENTIAL).
Missing (in isoform Short).
MISSING (in isoform Short).
HTTGACTLAPPPERFELDVLACHCRYRASASAEP (in isoform Short).
FT10a-VSP_001156.
N-TIGA-VSP_001156.

FT10a-VSP_001156.
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COLLAGEN ALPHA 1 (XVIII) CHAIN.

ENDOSTATIN.

TSP N-TERMINAL.

TSP N-TERMINAL.

TRIPLE-HELICAL REGION 1 (COLI).

NONHELICAL REGION 2 (NC2).

TRIPLE-HELICAL REGION 2 (COL2).

NONHELICAL REGION 3 (COL2).

TRIPLE-HELICAL REGION 4 (COL4).

NONHELICAL REGION 4 (COL4).

TRIPLE-HELICAL REGION 4 (COL4).

NONHELICAL REGION 6 (COL4).

NONHELICAL REGION 6 (COL6).

NONHELICAL REGION 6 (COL6).

TRIPLE-HELICAL REGION 6 (COL6).

NONHELICAL REGION 7 (NC9).

TRIPLE-HELICAL REGION 9 (COL9).

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NONHELICAL REGION 9 (COL9).

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TRIPLE-HELICAL REGION 9 (COL9).

NONHELICAL REGION 10 (COL10).

TRIPLE-HELICAL REGION 10 (COL10).

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TRIPLE-HELICAL REGION 10 (COL10).

TRIPLE-HELICAL REGION 11 (NC11).
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                                                                                                        1348 INSPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSIVRRADRAAVFIVNL
                                                                                                                                                                       LNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNL
                                                                                                                                                     121 RDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY
  PWRADDILAGPPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVA
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MEDLINE=9425707; PubMed=8188673;
REDLINE=94245707; PubMed=8188673;
REDLINE=94245707; PubMed=8188673;
Primary Structure of the alpha 1 chain of mouse type XVIII collagen, partial structure of the corresponding gene, and comparison of the alpha 1 alpha 1 (XVIII) chain with its homologue, the alpha 1 (XV) collagen chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEDLINE=94240112; PubMed=8183894; Rehn M.V., Pihlajaniami T.; "Alpha I(XVIII), a collagen chain with frequent interruptions in the collagenous sequence, a distinct tissue distribution, and homology with type XV collagen."; Proc. Natl. Acad. Sci. U.S.A. 91:4234-4238(1994).
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MEDLINE=21217748; PubMed=11321448;
Jia S., Zhu F., Li H., He F., Xiu R.-J.;
"Anticaneer treatment of endostatin gene therapy by targeting tumor neovasculature in C57/BL mice.";
Clin. Hemorheol. Microcirc. 23:251-257(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE-896455922; PubMed-8988009,
Rehn M., Hintikka E., Pihlajaniemi T.;
"Characterization of the mouse gene for the alpha-1 chain of type
"Characterization from one gene for the alpha-1 chain of type
"Characterization from seveals that the three variant N-terminal
polypeptide forms are transcribed from two widely separated
promoters.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                           CAIH MOUSE STANDARD; PRT; 1774 AA.
P39051; Q60672; Q61437; Q62001; Q62002; Q9JK63;
01-FBB-1995 (Rel. 31, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
COllagen alpha I (XVIII) chain precursor [Contains: Endostatin]
COL18A1.
                                                                                                                                                                                                                                                     1468 CETWRTEAPSATGQASSLLGGRLLGQSAASCHHAYIVLCIENSFMTA 1514
                                                                                                                                                                                                                              181 CETWRIEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMTS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 91:4229-4233(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cnain.";
J. Biol. Chem. 269:13929-13935(1994).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Mouse)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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EMBL, 103714; AAA20657.1;

EMBL, 103715; AACS2901.1; JOINED.

EMBL, 1034609; AACS2901.1; JOINED.

EMBL, 1034609; AACS2901.1; JOINED.

EMBL, 1034610; AACS2901.1; JOINED.

EMBL, 1034611; AACS2901.1; JOINED.

EMBL, 1034613; AACS2901.1; JOINED.

EMBL, 103716; AACS2901.1; JOINED.

EMBL, 103716; AACS2901.1; JOINED.

EMBL, 1034609; AACS2902.1; JOINED.

EMBL, 1034609; AACS2902.1; JOINED.

EMBL, 1034609; AACS2902.1; JOINED.

EMBL, 1034610; AACS2902.1; JOINED.

EMBL, 1034610; AACS2902.1; JOINED.

EMBL, 1034611; AACS2902.1; JOINED.

EMBL, 1034612; AACS2902.1; JOINED.

EMBL, 1034613; AACS2902.1; JOINED.

EMBL, 1034613; AACS2902.1; JOINED.

EMBL, 103716; AACS2903.1; JOINED.

EMBL, 1034601; AACS2903.1; JOINED.
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X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF ENDOSTATIN.
MEDLINE=99169382; Pubmed=9501097;
Hohenester E., Sasaki T., Olsen B.R., Timpl R.;
Crystal structure of the anglogenesis inhibitor endostatin at 1.5-A

[6] CHARACTERIZATION OF ENDOSTATIN, AND PARTIAL SEQUENCE. MEDLINE=97160848; PubMed=9008168; O'Reilly M.S., Boehm T., Shing Y., Fukai N., Vasios G., Lane W. Flynn E., Birkhead J.R., Olsen B.R., Folkman J.; "Endostatin: an endogenous inhibitor of angiogenesis and tumor

growth."; Cell 88:277-285(1997).

AGDRIEVONGAGUSGENCVPIGPAA -> MAPRWHILDU LISUVLLUNRVSWARP (in isoform 3).
LTSIVLLINRVSWARP (in isoform 3).
FITIG=VSP 001158.
Missing (in isoform 2).
FITIG=VSP 008303.
FITIG=VSP 008303.
P -> L (IN REF 4).
A -> R (IN REF 4). TRIPLE-HELICAL REGION 1 (NC1).
TRIPLE-HELICAL REGION 2 (NC2).
TRIPLE-HELICAL REGION 2 (CCL2).
TRIPLE-HELICAL REGION 3 (CCL2).
TRIPLE-HELICAL REGION 3 (CCL2).
TRIPLE-HELICAL REGION 4 (CCL3).
TRIPLE-HELICAL REGION 4 (CCL4).
TRIPLE-HELICAL REGION 6 (NC5).
TRIPLE-HELICAL REGION 6 (NC5).
TRIPLE-HELICAL REGION 6 (NC6).
TRIPLE-HELICAL REGION 6 (NC6).
TRIPLE-HELICAL REGION 7 (CCL5).
NONHELICAL REGION 7 (CCL6).
NONHELICAL REGION 9 (CCL6).
NONHELICAL REGION 9 (CCL6).
NONHELICAL REGION 9 (CCL9).
TRIPLE-HELICAL REGION 10 (NC10).
TRIPLE-HELICAL REGION 10 (NC10).
TRIPLE-HELICAL REGION 10 (CCL10).
NONHELICAL REGION 10 (CCL10).
NONHELICAL REGION 10 (CCL10).
NONHELICAL REGION 10 (CCL10).
NONHELICAL REGION 11 (NC11).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL). CELL ATTACHMENT SITE (POTENTIAL). Missing (in isoform 3). /FTId=VSP_001157. COLLAGEN ALPHA 1 (XVIII) CHAIN. TSP N-TERMINAL. FZ. 1194 DOMAIN CARBOHYD CARBOHYD CARBOHYD CARBOHYD DISULFID DISULFID CONFLICT CONFLICT CONFLICT VARSPLIC VARSPLIC VARSPLIC CHAIN DOMAIN CHAIN

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Proc. Natl. Acad. Sci. U.S.A. 89:10144-10148 (1992).

-I TISSUE SPECIFICITY: Expressed predominantly in internal organs

such as advental gland, pancreas and kidney.

-I PTM: Prolines at the third position of the tripeptide repeating

unit (G-X-Y) are hydroxylated in some or all of the chains.

-I SIMILARITY: BELICOG TO THE FIRRIL-ASSOCIATED COLLAGENS WITH

INTERRUPTED HELICES (FACIT) FAMILY.

-I SIMILARITY: COLTAIN 1 TSP N-terminal (TSPN) domain.

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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                  1548 PWRADDÍLÁNPPRLPDRÓPYPGVPHHHSSYVHLPPARPT----LSLAHTHQDFQPVLHLV 1603
                                                                                                                                                                                                                                                                                                                                        60 ALNSPOPGGMRGIRGADFQCPQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRIGVPVVN 119
                                                                                                                                                 1 PWRADDILAGPPRILDPOPYPGAP-HHGSYVHFOPARPTGGPVHTHTHTHQDFQLVLHLV
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MEDLINE=94148920; PubMed=8106446;
Kivirikko S., Heinamaki P., Rehn M.V., Honkanen N., Myers J.C.,
Pihlajaniemi I.;
Primary structure of the alpha 1 chain of human type XV collagen and
exon-intron organization in the 3' region of the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB-Placenta;
MEDIATNE-94140817; BubMed=8307960;
MEDIATNE-94140817; BubMed=8307960;
MULTAGE 1, Abe N. Winomiya Y., Olsen B.R., Ooshima A.;
"The human alpha 1(XV) collagen chain contains a large amino-terminal non-triple helical domain with a tandem repeat structure and homology to alpha 1(XVII) collagen.";
To alpha 1(XVII) collagen.";
J. Biol. Chem. 269:4042-4046(1994).
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MEDLINE-93066196; PubMed≈1279671;
Myers J.C., Kivirikko S., Gordon M.K., Dion A.S., Pihlajaniemi T.;
"Identification of a previously unknown human collagen chain, alpha
I(XY), characterized by extensive interruptions in the triple-helical
region.";
                                                                        5; Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 YCETWRTBAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMTSFSK 230
Query Match 79.4%; Score 983.5; DB 1; Length 1774; Best Local Similarity 80.1%; Pred. No. 6.3e-79; Matches 185; Conservative 18; Mismatches 23; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Collagen alpha 1(XV) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene.";
J. Biol. Chem. 269:4773-4779(1994).
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1233 ----ADFQCFKQARAAGLLSTYRAFLSSHLQDLSTIVRKAERYSLPIVNLKGQVLFNNWD 1288
                         131 ALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSYCETWRTEAPA 190
                                                                                 1349 VTGLASPLSTGKILDQKAYSCANRLIVLCIENSFMTDARK 1388
                                                                  191 ATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMTSFSK 230
                                                                                                                                               PRT; 547 AA
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                                                                                                                                               STANDARD;
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         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 PPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVALNSPQPGGMR 70
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non-profit institutions as long as its content is in
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InterPro; IPR008085; CorA like lec_gl.
InterPro; IPR001791; Laminin_G_
InterPro; IPR001199; TSPN.
Pfam; PF002109; TSPN;
Pfam; PF02210; TSPN;
SWART; SW00210; TSPN; 1.
SWART; SW00210; TSPN; 1.
SWART; Concetive tissue; Repeat; Hydroxylation; Cell adhesion; Collagen; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                   COLLAGEN ALPHA 1 (XV) CHAIN.
TSP N-TERMINAL.
NONHELICAL REGION 1 (NCL).
TRIPLE-HELICAL REGION 2 (NC2).
NONHELICAL REGION 2 (NC2).
NONHELICAL REGION 3 (COL2).
TRIPLE-HELICAL REGION 3 (COL2).
TRIPLE-HELICAL REGION 4 (NC3).
TRIPLE-HELICAL REGION 4 (NC4).
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WONDHELICAL REGION 8 (NC8).
TRIPLE-HELICAL REGION 9 (NC9).
NONHELICAL REGION 9 (NC9).
NONHELICAL REGION 9 (NC9).
NONHELICAL REGION 10 (NC10).
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                                                                                                                                                                                                                                                                                                                                                                                       NONHELICAL REGION 6 (NC6).
TRIPLE-HELICAL REGION 6 (COL6).
NONHELICAL REGION 7 (NC7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 10 C -> S (IN REF. 2).
49 49 D -> V (IN REF. 2).
95 5 L -> A (IN REF. 2).
150 150 P -> A (IN REF. 2).
204 204 M -> V (IN REF. 2).
409 409 0 R -> A (IN REF. 2).
1388 AA, 141930 MW; 60822AD925A3093D CRC64;
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                                             EMBL; 125286; AAA58429.1; -...
EMBL; D21230; BAA4762.1; -...
EMBL; L01697; -; NOT_ANNOTATED_CDS.
PIR, A53317; A53317.
HSS9; P99061; IXOR.
                                                                                                           Genew; HGNC:2192; COL15Al.
MIM; 120325; -.
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 PIPGS----SKAYREVANPDGGPSLRVPFRRVHLSTGAHFDLYDTSGPYTDPDAVINLTA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21128732; PubMed-=11234002;
Cole S.T., Biglineier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:1007-1011(2001).
-!- FUNCTION: Required for the synthesis of the hydromethylpyrimidine
-!- FUNCTION: Required for the synthesis of the hydroxymethylpyrimidine (4-amino-2-methyl-5-
hydroxymethylpyrimidine) (By similarity).
-!- PATHWAY: Thiamine biosynthesis.
-!- SIMILARITY: Belongs to the thiC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Gaps
                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 7.5%; Score 93.5; DB 1; Length 547; Similarity 27.4%; Pred. No. 0.87; Conservative 14; Mismatches 49; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL035159; CAA22712.1; -.
EMBL; AL683918; CAC29802.1; -.
EMBL; AL683918; CAC29802.1; -.
EMBL; AL0294; -.
Leproma, ML0294; -.
HAWAP; MF 00089; -; 1.
Interproj IPR002817; Thic.
Probom; PP01964; Thic; 1.
From; PP007048; Thic; 1.
TIGREPAMS; IGR00190; thic; 1.
TIGREPAMS; IGR00190; thic; 1.
THIGREPAMS; CACA97Theeds; Complete protecome.
SEQUENCE 547 AA; 59840 MW; 797DFB09DE462D58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Thisamine biosynthesis protein thic.
Mycobacterium leprae.
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61 GG-----AADGSRFSTPRGAGKLGKKRALSISPLSDSSVDLQTVIRTSPNSLVAPINSRC 115

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNL 120
                                    73 GLPPRPGVIRD-RGTQ---LQRARAGEITAEM-AFI-----ADREGMPAELV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 POPYPGAPH-----HGSYVHFOPARPTGGPVHTH----THTHODFQLVLHLVALNSPQP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         during limb development.";
Dev. Biol. 180:273-283 (1996)
-!- FUNCTION: MAY REGULATE THE TRANSCRIPTION OF SPECIFIC GENES DURING
-!- FUNCTION: MAY REGULATE THE TARANSCRIPTION OF SPECIFIC GENES DURING
NORMAL DEVELOPMENT. MAY PLAY A ROLE IN CRANIOPACIAL DEVELOPMENT
AND DIGITAL DEVELOPMENT. AS WELL AS DEVELOPMENT OF THE CENTRAL
NERVOUS SYSTEM AND GASTROINTESTINAL TRACT. IMPLICATED IN THE
TRANSDUCTION OF SHH SIGNAL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves; Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

BEDLINES-105842; Pubmed=8948590;

Marigo V., Johnson R.L., Vortkamp A., Tabin C.J.;

Marigo V., Johnson R.L., Vortkamp A., Tabin C.J.;

"Sonic hedgehog differentially regulates expression of GLI and GLI3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR007067, Znf C2H2.
Pfam: PF00056; zf-C2H3, 5.
SMARY, SN00355, ZnF C2H2, 5.
PROSITE: PS00029; ZINC_FINGER_C2H2_1; 4.
PROSITE: PS50157; ZINC_FINGER_C2H2_2; 5.
Zinc-finger; Metal-binding; DNA-binding; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE GLI FAMILY OF C2H2-TYPE ZINC-FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.3%; Score 90; DB 1; Length 556;
26.0%; Pred. No. 1.8;
ive 22; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 337 C2H2-TYPE.

343 368 C2H2-TYPE.

574 399 C2H2-TYPE.

556 556 556 556 556 AA; 60215 MW; 722D2AA5A1CA4D98 CRC64;
                                                                          121 RDEVLF------PSWEALFSGSEGQLKPGARI 146
                                                                                                               115 RVEVALGRAVIPANHNHPEIEPMIIGKAFAVKVNANI 151
                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein GLII (GLI) (Fragment)
GLII OR GLI.
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C2H2-TYPE.
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ZN FING 247 272
                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken)
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                                                                                                                                                                                                           GLI CHICK
P55878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZN FING
NON TER
SEQUENCE
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67 GGMRGIRGADFQCFQQARAAGLAGTFRAF----LSSRLQDLYSIVRRADRIGVPVVNLRD 122

7 PÓAR PYAEHCCPRPLHGASAGTPGLQGLDFPV-CHQPNLASSHHGYGLV----PGTEHP 60

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7.1%; Score 88; DB 1; Length 1233;
26.6%; Pred. No. 6.8;
ive 15; Mismatches 93; Indels 66; Gaps 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1037 RSGRPFL----PLFPELEDLPLLGKEQL---AR-----REALLHAAWAR-----GSRP 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    977 PPGRPPTPGPPLSDVSRVSRRPAWEÅRWPVRTGHCGRHLSASERPLSPARCHYSSFPRÅD 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 RTGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLOHPAWPRKSVWHGSDP 171
                                                                                                                                                                                                                                                                                                                                                                                                               940 SGÞSPCLPTPDÞPFBPSPTGWGP-----ÞDGGRA------ALVRRAÞQ 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGGMRGIRGADFQCFQ-----QARAAGLAGTFRAFLSSRLQDL----YSIVRRAD 111
                                                                                                                                                                                                                                                                                                                                                                           9 AGPPRLL---DPOPYPGAPHHGSYVHFQPARPTGGPVHTHTHQDFQLVLHLVALNSPQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1078 RHASLPSSVABAFARPSSLPAGCTGPACARPDGHSACRRLAQAQSMCLPIYREACQE 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 SGRRLIDSYCETWR--TEAPA-ATGOASSLLAG----RLLEGEAASCRHAFVVLCIE 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

TISSUB=Brain, and Cerebellum;

MEDLINE=95038818; PubMed=7951322;

Banfi S., Servadio A., Chung M.-Y., Kwiatkowski T.J. Jr., McCall A.E.

Duvick L.A., Shen Y., Robh E.J., Orr H.T., Zoghbi H.Y.;

"Identification and characterization of the gene causing type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEGUENCE OF 189-231 FROM N.A.
MEDLINE-96177682; PubMed-8634720;
Quan F., Janas J., Popovich B.W.;
"A novel CAG repeat configuration in the SCAI gene: implications for the molecular diagnostics of spinocerebellar ataxia type 1.";
Hum. Mol. Genet. 4:2411-2413(1995).
                                                                                  1 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
4 (POTENTIAL).
FUNCTIONAL DETERMINANT OF NADA RECEPTORS (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Receptor; Signal; Transmembrane; Postsynaptic membrane; Calcium;
                                  POTENTIAL.
GLUTAMATE [NMDA] RECEPTOR SUBUNIT
EPSILON 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tubby B.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATX1 HUMAN STANDARD; PRT; 816 AA.
PS4253; O9UG2; O9Y471;
O1-OCT-1996 (Rel. 34, Created)
O1-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ataxin-1 (Spinocerebellar ataxia type 1 protein).
SCA1 OR ATX1.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nat. Genet. 7:513-519(1994).
                                                                                                                                                                                                                                                                                                                         Local Similarity 26.6%
les 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spinocerebellar ataxia."
                 Ionic channel; Magnesium.
SIGNAL 1 19
CHAIN 20 1233
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SELF-ASSOCIATION SITE.
                                                                                                                                                                                               70 7
337 33
438 43
539 53
1233 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 63
                                                                                    TRANSMEM
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SITE
                                                                                                                                                                                                                                                      CARBOHYD
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                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease.
--- DISEAS: Defects in SCAl are the cause of spinocerebellar ataxia type 1 (SCAl) [MIM:164400]; also known as olivopontocerebellar atrophy I (OPCA I). SCAl is an autosomal dominant neurodegenerative disorder characterized by progressive neuronal loss in the cerebellum, brain stem and spinocerebellar tracts. Clinical features are cerebellar ataxia, dysarthria, ophtalmoparesis, muscle wasting and neuropathy. Onset of the disease usually occurs in the third or fourth decade of life and death occurs ten to twenty years later.
--- MISCELLANEOUS: The self-association seems to be necessary to form nuclear aggregates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR003652; Atax....
SWART; SM0536; AXH; 1.
RNA-binding; Nuclear protein; Polymorphism; Triplet repeat expansion;
Alternative splicing.
POLY-GLN.
DOMAIN 197 226
REI.P-ASSOCIATION SITE.
                                                                                                                                                                                                                                                                                                                                                                                               Name=1; sequence=Displayed; Isodoportion to body.
--- TISSUE SPECIFICITY: Widely expressed throughout the body.
--- POLYMORPHISM: The poly-Gin region of SCA1 is highly polymorphic (--- POLYMORPHISM: The poly-Gin region of SCA1 is highly polymorphic (--- 23) repeats) in the normal population and is expanded to about 40-83 repeats in scal patients. Longer expansions result in earlier onset and more severe clinical manifestations of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%; Score 87.5; DB 1; Length 816; 22.4%; Pred. No. 4.7; ative 26; Mismatches 96; Indels 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495 605 SELF-ASSOCIATION SITE.
541 767 RNA BINDING.
795 798 NUCLEAR LOCALIZATION SIGNAL
816 AA, 87051 MW; D49BA5D5423D0777 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EWBL; X79204; CAA55793.1; --
EWBL; AL009031; CAA15622.1; --
EWBL; 802497; AAD14401.1; --
FIR; 546268; S46268.
Genew; HGNC:10548; SCA1.
MIM; 601556; --
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005737; C:cytoplasm; TAS.
SMART; SM00536; AXH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 22.4
Matches 54; Conservative
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Gaps

92 ;

[5]
RNA-BINDING DOWAIN.
MEDLINE=21065637; PubMed=11136710;
Yue S., Serra H.G., Zoghbi H.Y., Orr H.T.;
"The spinocerebellar ataxia type 1 protein, ataxin-1, has RNA-binding activity that is inversely affected by the length of its polyglutamine

"Identification of a self-association region within the SCA1 gene

product, ataxin-1."; Hum. Mol. Genet. 6:513-518(1997)

MEDLINE=97252384; PubMed=9097953; Burright E.N., Davidson J.D., Duvick L.A., Koshy B., Zoghbi

12011

Hum. Mol. Genet. 10:25-30(2001).
-!- FUNCTION: Binds RNA in vitro. May be involved in RNA metabolism.
-!- FUNCTION: Binds RNA in vitro. May be involved in RNA metabolism.
-!- SUBUNIT: Interacts with LANP and AlU.
-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing, Named isoforms=1; Comment=At least 2 isoforms are produced;

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                                     228 ISRAPGLITPGSPPPA-QONOYVHISSSPQNTGRTASPPAIPVHLHPHQ----TMIPHTL 282
                                                                                                                        283 TLGPPSQVVMQYADSGSHFVPREATKKAE-----SRLQQAIQAKEVLNGEMEKSR 333
                                                                                                                                                                     112 RIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARI - - FSFDGRDVLQHPAWPRKSVWHGS 169
                                                                                                                                                                                                   334 RYGAP-----SADLGLGKAGGKSVPHPYESRHVVVHPS---PSDYSSR 374
                                                                                                                                                                                                                                                          170 DPSGRRLT-------DSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAF 215
                                                                                  ALNSPOPGGMR-GIRGADFOCFOOARAGLAGTFRAFLSSRLOD-----LYSIVRRAD 111
                                                                                                                                                                                                                                                                                                       375 DPSGVRASVMVLPNSNTPAADLEVQQATHREASPSTLNDKSGLHLGKPGHRSYALSPHTV 434
8 LAGPPRILIDPQPYPGAPHHGSYVHF-----QPARPTGGPVHTHTHTHQDFQLVLHLV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAINSATCC 15692 / PAOL;
MEDLINE=20437337, PubMed=10984043;
MEDLINE=2043737, PubMed=10984043;
MEDLINE=2043737, PubMed=10984043;
MICOGNOINE=2043737, PubMed=10984043;
MICOGNILE R.O., Establing B.O., Kowalik D.J., Lagrou M., Garber R.L., Gollery L., Tolenting E., Westbrock-Wadman S., Yuan Y., Garber R.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAOL, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94124011; PubMed=8294014;
Maharaj R., May T.B., Wang S.-K., Chakrabarty A.M.;
Sequence of the alg8 and alg44 genes involved in the synthesis of
alginate by Peeudomonas aeruginosa.";
Gene 136:267-269(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mannironic acid.
--- PATHWAY: Alginate biosynthesis.
--- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
--- SIMILARITY: Belongs to the glycosyltransferase family 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- FUNCTION: Possibly a processive enzyme that polymerizes GDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L22611; AAC36875.2; ALT_INIT.
EMBL; ABC04774; AAG06829.1; -.
PIR; A83204; A83204; A83204.
Alginate biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q52463; Q9HY70;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycosyl transferase alg8 (EC 2.4.1.-).
ALG8 OR PA3541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                               216 V 216
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                                                                                                                                                                                                                                                                                         133 FSGSEGQLKPGARIFS-----FDGRDVLQHPAWPRKSVWHGSDPS-GRRLTDS 179
                                                                                                                                                                                                                                                      99 IDALITAMYYRSVIREAIDSGYPTTVVCSIVEMSDEVLVRSLWRKMNPPDRVSLDFVRIP 158
                                                                                                                                                                                                                                                                                                                          159 GTGKRDGLAYGFRAISRHLPDDDAVVAVIDGDTVLDHGVVKKTVPWFKLPPNVGGLTTNE 218
                                                                                                                                                    66
                                                                                                                                                                                     æσ
                                                                                                                                                    50 QDFQLVLHLVALNSPQPGGMRGIRGADF------QCFQQARAAGLAGTFRAFLSSR
                                                                                                                                                                                   39 KDFILLIGAVGIWRYSMGGVHFLRGMLFLHVVYPYYRRRVRQLGSAADPSHVFLMVTSFR
                                                                                                                                                                                                                        100 LQDL-----YSIVRRADRTGVP-----VVNLRDEVLFPS-WBAL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., Tabera S.;
                                                                                                                    50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Homogentisicase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                   DB 1; Length 494;
                                                                                                                    68; Indels
381 403 POTENTIAL.
423 445 POTENTIAL.
115 115 A -> R (IN REF. 1).
494 AA; 56456 MW; D89A5627E913FDF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Homogenisate 1,2-dioxygenase (EC 1.13.11.5) (Homogent (Homogentisate 1,2-dioxygenase) (Homogentisic acid oxidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 AA.
                                                                                                                    20; Mismatches
                                                                                   Score 87;
                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP005936; BAC45608.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22484998; PubMed=12597275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF_00334; -; 1.
InterPro; IRR0057113; Cupin_sup.
InterPro; IRR005708; HmgA.
Pfam; PF04209; HgmA; 1.
                                                                                     7.0%;
                                                                                                  24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bradyrhizobium japonicum.
                                                                                                                    45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             180 YCE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMGA OR BLL0343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BRAJA
                                                                                 Query Match
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HGD_BRAJA
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Complete proteome

Transmembrane;

TRANSMEM TRANSMEM TRANSMEM TRANSMEM

WFFFFF S

34 71 445

SEQUENCE

us-09-938-391-2.rsp

POTENTIAL

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STANDARD;
                20
31
266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                 321
                                                                                                                                                                                                                                                                                                                                                                                                                      CHRD MOUSE
                                                                              ACT SITE
SEQUENCE
                                                                                                                     Query Match
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CHAIN
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Matches
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                                                                                                                                                9.
                                                                                                                                                                                                                         76 DEQCEQQARAAGLAGTERA-----FLSSRLQDLYSIVRRADRIGVP-VVNLRDEVL--F 126
                                                                                                                                                                                                                                                                             PSWEALFSGSEGOLKP----GARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSYCE 182
                                                                                                                                                                                        325 DEVIEPE-RWMVADNTERPEWYHMNIMSEFMGLIYGVYDAKPQGFVPGGMSLHNCMLPHG 383
                                                                                                                                                                                                                                                                                             24 PH-----HGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVALNSPQPGGMRGIRGA 75
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10

NRT1_CHICK STANDARD; PRT; 312 AA.

AC 055806;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE NAD(P) (+) -- arginine ADP-ribosyltransferase 1 precursor (BC 2.4.2.31)

DE (Mono (ADP-ribosyl transferase 1) (ATI).

OS Gallus gallus (Chicken).

CE Laryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=White leghorn; TISSUE=Bone marrow;

BIDLINES-25050487; PubMed-7961689;

Tsuchiya M., Hara N., Yamada K., Osago H., Shimoyama M.;

Tsuchiya M., Hara n., Yamada K., Osago H., Shimoyama M.;

"Cloning and expression of cDNA for arginine-specific ADP-
"Insorptransferase from chicken bone marrow cells.";

J. Biol. Chem. 269:27421-27457 (1994).

-i. CATALYTIC ACTIVITY: NAD(+) + L-arginine = nicotinamide + N(2)-
TIGRFAMS; TIGRO1015; hmgA; 1.

Oxidoreductase; Dioxygenase; Metal-binding; Iron;
Phenylalanine catabolism; Tyrosine catabolism; Complete proteome.
METAL
METAL
346 346 1RON (BY SIMILARITY).
METAL
352 352 IRON (BY SIMILARITY).
METAL
352 352 IRON (BY SIMILARITY).
METAL
36780 MW; F6DD465E68735D3C GCG4;
                                                                                                                   6.9%; Score 86; DB 1; Length 448; 24.0%; Pred. No. 3.2; tive 25; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A55461; A55461.
InterPro; IPR000768; ART.
Pfam, PP01129; ART; 1.
PRINTS; PR00970; RIBTRNSFRASE.
PROSITE; P801291; ART; 1.
Transferase; Glycosyltransferase; NAD; Signal; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D31864; BAA06664.1; ~.
                                                                                                                                                44; Conservative
                                                                                                                        Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                    TWR 185
                                                                                                                                                                                                                                                                                                                                                              CWK 437
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                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                              81 QQARAAGLAGTERAFLSSRL-----QDLYSIVRRADRTGVPVVNL-----RDEVLF 126
                                                                                                                                                                                                                                                                                                                                                                                                  172 MIQR--GKSVRFGQFTSISLRKEATVNFGQDTIFVVKTC--YGVPIKQFSFFPSEDEVLI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 PSWEAL----FSGSEGQ-----LORINGARIFSFDGRDV-----LOH 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 PPFEVFEVINFSNDRGSVKIQLHSKGKMSTHNCELLKPQGGQWGRGHQEVGLGLSPGLSL 287
                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 ENEATROGGRSHODYIHSYHFKTLHFFLTQALFALRASQPRCYYVYRGVRGIR-----F
                                                                                                                                                                                                                                                      32 FOPARPTGGPVH-THTHTHQ----DFQLVLHLVALNSPQP-----GGMRGIRGADFQCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mu
                                                                                                                                                                                                         70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEGUENCE FROM N.A.
Pappano W.N., Scott I.C., Clark T.G., Eddy R.L., Shows T.B.,
Greenspan D.S.,
                                                                                                                                              ch 6.9%; Score 85; DB 1; Length 312; I Similarity 26.5%; Pred. No. 2.6; 53; Conservative 15; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=B6SJL/F1;
In B., Bachiller D., Agius E., Piccolo S., De Robertis E
In B., Bachiller D., Agius E., Piccolo S., De Robertis E
"BMP-binding domains in the chordin secreted protein.",
submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                               POTENTIAL.
BY SIMILARITY.
B82980439BC904FC CRC64;
NAD(P)(+)--ARGININE ADP-
                      RIBOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the chordin family. SIMILARITY: Contains 4 CHRD domains. SIMILARITY: Contains 4 VWFC domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      948 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 PAWP-RKSVWHG----SDP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 PVLPCKRRVWEGLGHREGDP 307
                                               267 312 P
231 231 B
312 AA; 35318 MW;
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STRAINEATCO.

STRAINEATCC 90305 / SB111;

STRAINEATCC 90305 / SB111;

MEDLINE=20138231; PubMed=10671527;

Cheng Y:-0., Walton J.D.;

"A elikaryotic alanine racemase gene involved in cyclic peptide
biosynthesis.";

"J. Biol. Chem. 275:4906-4911(2000).

-:-FUNCTION: Non-ribosomal peptide synthetase, able to activate
profine and ABO (2-amino-9,10-epoxia-8-oxodesanoic acid), and
primerize L.Pro. Catalyzes the production of HC-toxin: a cyclic
tetrapeptide. Activates and thioesterifies L-Pro, and epimerizes
it to D-FRO; also uses D-Ala as a substrate but this is epimerized
   filamentous fungus Cochliobolus carbonum is encoded by 15.7-kilobase open reading frame."; J. Biol. Chem. 267:26044-26049(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M98024; AAA33023.1; -.
HSSP; P14687; 1AMU.
     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 ---LIGPRSQAVARARVSLLRSSLRFSVSYQRLDRPSRVRFTDFIG-----NILF-- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 LDPQPAGLVFEYPRDPEHRSY---SDRGEPGVGERTRADGHTDF-----VÅL----- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 MRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNLRDEVLFPS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EHPATPTQDGLVCGVWRAVPRLSVRLLRA--EQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 WEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRK-----SVWHGSDPSGRRLTDSYCET 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 LDPQP-----YPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVALNSPQPGG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC, .,) (POTENTIAL), N-LINKED (GLCNAC, .,) (POTENTIAL), N-LINKED (GLCNAC, .,) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 84; DB 1; Length 948; 84.2%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 24.2%; rreu. No. 11.
Matches 53; Conservative 17; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101512 MW; 4DC2DA01D9BD2147 CRC64;
                                                                                                                                                                                                                                                                                         at, Glycoprotein; Signal.
POTENTIAL.
CHORDIN.
VWFC 1.
CHRD 2.
CHRD 3.
CHRD 3.
CHRD 4.
VWFC 2.
VWFC 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 WRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIEN 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Se
or send an email to license@isb-sib.ch),
                                                EMBL; AF096276; AAD19895.1; ..
EMBL; AF069501; AAC68867.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     948 AA;
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CARBOHYD
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CARBOHYD
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AC 001886

DT 01-FEB

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1713 PKRPTNVKAGEBE-------HHLCFESLSMSDPT-------EFDLTLFV-- 1747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PWRADDILAGPPRILDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.7%; Score 82.5; DB 1; Length 5217;
24.9%; Pred. No. 1.18+02;
tive 15; Mismatches 72; Indels 43; Gaps
# HSSP; Pl4647; 1AMC

# GO; GO: 00016881; F:acid-D-amino acid ligase activity, IDA.

# GO; GO: 000403; P:toxin biosynthesis; IDA.

# InterPro; IPR000873; AMP-bind.

# InterPro; IPR006163; Pp_bind.

# InterPro; IPR006124; Condensation; S.

# PR051TE; PS00012; PH05PD-DATATHEINE; 4.

# PR051TE; PS00012; PH05PD-DATATHEINE; RPD-DATATHEINE; RPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 24.9%
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=ATCC 90305 / SB11;
MEDLINE=93100328; PubMed=1281482;
SCOCET-Craig J.S., Panaccione D.G., Pocard J.-A., Walton J.D.;
"The cyclic peptide synthetase catalyzing HC-toxin production in the

Bukaryota, Fungi, Ascomycota, Pezizomycotina, Dothideomycetes, Pleosporales, Pleosporaceae, Cochliobolus.

NCBI_TaxID=5017;

Cochliobolus carbonum (Bipolaris zeicola)

01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) HC-toxin synthetase (EC 6.3.2.-) (HTS),

STANDARD;

HTS1 COCCA

119 NLRDEVLFPSWEALFSGSEGQLKPGAR--IFSFDGRDVLQHPAWPRKSVWHGS 169

1011 Fight 49 1/.34.40

1 PWRADDILAGPPRLLDPQ----PYP----GAPHHGSYVHFQP-----

8

finger domains ";

finger domains ";

Proc. Nall, Acad. Sci. U.S.A. 88:10079-10083(1991).

- FUNCTION: Transcriptional regulator (By similarity).

- FUNCTION: Transcriptional regulator (By similarity).

- FUNCTION: BY PHA/PMA OR BY SERUM.

- INDUCTION: BY PHA/PMA OR BY SERUM.

- SIMILARITY: BELONGS TO THE EGR FAMILY OF C2H2-TYPE ZINC-FINGER

PROTEINS.

- SIMILARITY: Contains 3 C2H2-type zinc fingers.

- FINITARITY: Contains 3 C2H2-type zinc fingers.

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MEDLINE=99278383; PubMed=8504297;
HOIST C., Skerka C., Lichter P., Bialonski A., Zipfel P.F.;
"Genomic organization, chromosomal localization and promoter function of the human zinc-finger gene pAT133.";
Hum. Mol. Genet. 2:367-372(1993). MEDLINE=92052214; PubMed=1658795; Mueller H.-J., Seerka C., Bialonski A., Zipfel P.F.; "Chone pAT133 identifies a gene that encodes another human member of a class of growth factor-induced genes with almost identical zinc-Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update) Early growth response protein 4 (EGR-4) (AT133). 486 AA STANDARD; Homo sapiens (Human). SEQUENCE FROM N.A. finger domains." EGR4 HUMAN Q05215; STATE THE TENERS BEING BELL OF THE STATE TO THE STATE TO THE STATE

DR EMBL; X69438; CAA49214.1; -.

DR EMBL; X69438; CAA49214.1; -.

DR EMBL; X60146, CAA42698.1; -.

DR EMBL; X60146, CAA42698.1; -.

DR EMBL; X60146, CAA42698.1; -.

DR TRANSRAC; T05190; -.

DR TRANSRAC; T05190; -.

DR GO: 00002844; PEDOSitive regulation of cell proliferation; TAS.

DR GO: 00002844; PEDOSitive regulation of cell proliferation; TAS.

DR GO: 00002844; PEDOSitive regulation of cell proliferation; TAS.

DR FAML; PRO0056; ZE-CZH2; 1.

DR ProDom; PD000003; Znf CZH2; 1.

DR PROSITE; PS00105; ZINC_FINGER CZH2; 1.

DR PROSITE; PS00157; ZINC_FINGER CZH2 1; 3.

PROSITE; PS00157; ZINC_FINGER CZH2 2; 3.

RW NUCLEAR PROCEDI; TRANSTRIPION REGULATION; DNA-binding; Zinc-finger;

MACAI-binding; Repeat. CZH2-TYPE 1.

ZN FING 40 404 CZH2-TYPE 2.

ZN FING 410 432 CZH2-TYPE 2.

ET ZN FING 438 460 CZH2-TYPE 3.

FT ZN FING 438 460 CZH2-TYPE 3.

FT ZONFLICT 427 427 S. > T (IN REF. 2).

48;

6.6%; Score 82; DB 1; Length 486; llarity 24.6%; Pred. No. 7.9; Conservative 23; Mismatches 58; Indels

Query Match Best Local Similarity Matches 42; Conserv

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                                                                                                                    36 RPTGGPVHTHTHTHODFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                          96 LSSRLQDLYSIVRRADRIGVPVVNLRDEVLFPS--WEALFSGSEGQLKPGA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-RED-2004 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
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28-FEB-2003 (Rel. 41, Last annotation update)
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28-FEB-2003 (Rel. 41, Last annotation u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hunt A.;
Subjected (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUTLET(TION: May function as a GTPass-activating protein.
-!- SIMILARITY: Contains 1 Rho-GAP domain.
-!- SIMILARITY: Contains 1 START domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhodes S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     995 AA
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EMBL; 284483; CAC94774.1; --
EMBL; B9942; H9942.
Genew, HGMC:19164; STARD13.
InterPro; IPR008936; Rho GAP.
InterPro; IPR00198; RhoGAP.
InterPro; IPR00198; RhoGAP.
InterPro; IPR0020313; START.
Pfam; PF01620; RhoGAP; 1.
Pfam; PF01620; RhoGAP; 1.
SMART; SM00234; RhoGAP; 1.
PROSITE; PS00238; RTART; 1.
PROSITE; PS0034; START; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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989
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144 -----ARIFSFD----GRDVLQHPAWPRKSVWHGSDPSGRRLTDSY---CETWR 185
                                                     96 QCCTDNPVMLDAPLVSSSLPQPPRDVLNHPFHPK-----NEKPTRARAKSFLKRMFTLR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 GGCSHQYYVHFY------HFKT-LHFLLTQALFALRASQPRCYYVYRGVRGIR-- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 ----FMTQR--GKSVRFGQFTSTSLRKDVAVNFGQDTFFVVKTC--YGVPIKQFSFYPSE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 DFQCFQQARAAGLAGTFRAFLSSRL-----QDLYSIVRRADRTGVPVVNL----R 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 GAPHHGSYVHFQPARPTGGPVHTHTHTQDFQLVLHLVALNSPQP-----GGMRGIRGA 75
                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
NAD(P)(4)--arginine ADP-ribosyltransferase 2 precursor (EC 2.4.2.31)
(Mono(ADP-ribosyl) transferase 2) (AT2).
(Mono(ADP-ribosyl) transferase 2) (AT2).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ADP-D-ribosyl)-L-arginine.
-!- SUBCELLULAR LOCATION: THE MATURE EXZYME IS PROBABLY SECRETED FROM GRAUNLOCYTES INTO THE EXTRACELLULAR SPACE.
-!- SIMILARITY: Belongs to the Arg-specific ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=White leghorn, TISSUE=Bone marrow;
MEDLINE=$950504871; PubMed=7951658;
MEDLINE=$950504871; PubMed=7951658;
TSuchiya M., Hara N., Yamada K., Osago H., Shimoyama M.;
"Cloning and expression of cDNA for arginine-specific ADP-ribosyltransferase from chicken bone marrow cells.";
J. Biol. Chem. 269:27451_27451_0949;
-1- CATALYTIC ACTIVITY: NAD(+) + L-arginine = nicotinamide + N(2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6%; Score 81.5; DB 1; Length 312;
26.5%; Pred. No. 5.3;
tive 16; Mismatches 68; Indels 63
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                                                                                                                                                                    186 TEAPAATGQASS-----LLAGRLLEQEAASCRHAFVVLCIE 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9E45A9B7A6BC4057 CRC64;
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BY SIMILARITY.

NAD (P) (+) --ARGININE ADP-
RIBOSYLTRANSFERASE 2.
                                                                                                                                                                                                                                                                                                                                                             312 AA.
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BY SIMILARITY.
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PROSITE; PS01291; ART; 1.
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231 231 B
312 AA; 34966 MW;
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InterPro; IPR000768; ART.
Pfam; PP01129; ART; 1.
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                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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        Qy
        122 DEVLFPSWEAL---FSGSEGGLKPGARI---FSFDGRDVLQHPAWPRKSVW-HGSDPSG
        173

        Db
        223 DEVLIPPEVFEVTNFTGNGRIQIYLRSKGKWSRHNCELLK----PRGGQWGRGHQEVG
        278

        Qy
        174 RRLTD-----SYCETW
        184

        Db
        279 LGLSPGLALPVLPCSNCSCW
        298

        Search completed: March 26, 2004, 13:36:31
        36:31
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March 26, 2004, 13:32:37 ; Search time 40.5556 Seconds (without alignments) 1789.377 Million cell updates/sec
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1 PWRADDILAGPPRLLDPQPY......CRHAFVVLCIENSVMTSFSK 230
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
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sp_virus:*
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Gapop 10.0 , Gapext 0.5
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11:
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S		Description	Q8n4s4 homo sapien	O61434 mus musculu	O9gzd2 rattus norv	Ognal9 homo sapien	Q8wxi5 homo sapien	093419 gallus gall	O9wuw5 rattus norv	Osqhl9 xenopus lae	OBjff7 xenopus lae	Ogert2 mus musculu	Osawce brachydanio	035206 mus musculu	mus	c		
SUMMARIES								_		_	_				_			
SUM	4	77	Q8N4S4	061434	090ZD2	QBNG19	QBWXIS	093419	Q9WUWS	OBOHILS	QBJFF7	Q9CRT2	QBAWC6	035206	O9EQD9	Q9Y4W4	925980	096770
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Q8mt89 drosophila				Q9u9k6 caenorhabdi	Q9u9k7 caenorhabdi	Q8i0g6 caenorhabdi	Q89i38 bradyrhizob			Q53235 rhodobacter	Q7z107 recombinant	Q62700 rattus norv				Q92k28 rhizobium m	a	യ	052679 escherichia	œ	.0	-	4	Ω,	Q7y2x3 stx2 conver	4	Q88e70 pseudomonas	Q8scb2 stx2 conver
Q8MT89	Q8MSE3	Q86BH1	017866	Q9U9K6	Q9U9K7	QBIOGE	089138	Q82BY9	Q8P380	Q53235	Q7ZL07	062700	Q7ZL05	Q9ATK5	Q9VFA9	Q92K28	QBCJK2	052660	052679	083378	Q9VWS5	Q8LIQ7	Q9S0R7	О 9ХЛКЗ	Q7Y2X3	Q9KXC4	Q88E70	Qescb2
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ALIGNMENTS

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61 LNSPOPGGMRGIRGADFOCFOOARAGLAGTFRAFLSSRLODLYSIVRRADRIGVPVVNL 120
                                                                                                                                                                                                                                                                                                                                                                                                          121 RDEVLFPSWEALFSGSEGQLKFGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSY 180
                                                                                                                                                                                                                                                                                                                    1 PWRADDILAGPPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVA 60
                                                                                                                                                                                                                                                                                               4; Gaps
                  Query Match 82.2%; Score 1019; DB 4; Length 816; Best Local Similarity 82.4%; Pred. No. 1.8e-89; Matches 187; Conservative 16; Mismatches 20; Indels 4
                                                                                                                   TISSUERCE FROM N.A.
TISSUE-Renal adenocarcinoma;
Strausberg R.,
Submitted (Jul.-2002) to the EMBL/GenBank/DDBJ databases.
ENEL; BC03715; AAH33715.1; ...
InterPro; IPR008161; Clg.helix.
InterPro; IPR008160; Collagen.
Promp. P001991; Collagen.
Promp. P000007; Clg.helix; 1.
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815 AA, 82553 MW; 5D539B2946694F86 CRC64;
  PRT; 816 AA.
 PRELIMINARY;
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us-09-938-391-2.rspt

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1030 LKDEVLSPSWDSLFSGSQGQLQPGARIFSFDGRDVLRHPAWPQKSVWHGSDPSGRRLMES 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 ALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 LRDEVLPPSWEALFSGSEGOLKPGARIFSFDGRDVLOHPAWPRKSVWHGSDPSGRRLTDS 179
914 PWRADDILANPPRLPDRQPYPGVPHHHSSYVHLPPARPT----LSLAHTHQDFQPVLHLV 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PWRADDILAGPPRLLDPQPYPGAP-HHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abe N., Muragaki Y., Yoshioka H., Inoue H., Ninomiya Y.;

"Identification of a novel collagen chain represented by extensive interpretation of a novel collagen chain represented by extensive interpretations in the triple-helical region.";

I of 1. Mol. Biol. Res. 196:576-582(1993).

R DEN BSS-101. BSS-101.

R PIR, BSS-101. BSS-101.

R PRSP. P39061; IROB.

R GO; GO:0007155, P:cell adhesion; IBA.

R GO; GO:0007155, P:cell adhesion; IBA.

InterPro; IPR008160; Collagen.

R InterPro; IPR008160; Collagen.

R InterPro; IPR003129; TSPN.

R Pfam; PF02319; Collagen.

R Pfam; PF02310; TSPN; 1.
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79.4%; Score 983.5; DB 11; Length 1140;
Best Local Similarity 80.1%; Pred. No. 7.4e-86;
Matches 185; Conservative 18; Mismatches 23; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musimae, Mus
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                                                                               181 CETWRTEAPAATGOASSILAGRILEQEAASCRHAFVVLCIENSVMTS 227
                                                                                                              768 CETWRTEAPSATGQASSLLGGRLLGQSAASCHHAYIVLCIENSFWTA 814
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1140 AA; 115156 MW; 8B0C7E6862B3BDFE CRC64;
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01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-OCT-2002 (TYEMBLrel. 22, Last annotation update)
Collagen XVIII (Fragment).
                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                    PRT; 1140 AA
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                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                           Collagen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collagen.
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Q9QZD2
ID Q9QZD
AC Q9QZD
DT 01-M
DT 01-M
DT 01-OC
DE CO112
OS RALLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 NSPQPGGMRGIRGADFQCPQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNLR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 DEVIFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSYC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 DEVLSPSWDTLFSGSGSQLHSGARIFSFDGRDVLRHPAWPQKSVWHGSDPSGRRLMESYC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 PRKLYD---YGGGSGGGS-----GGGSGG-----GHSHRDFQPVLHLVALNSPLSGGMR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 GIRGADFOCFOGARAGLAGTFRAFLSSRLODLYSIVRRADRIGVPVVNLRDEVLFPSWE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 PPRILIDPQPYPGAPHHGSYVHFQPARPIGGPVHTHTHTHQDFQLVLHLVALNSPQPGGMR 70
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.4%; Score 897.5; DB 11; Length 226; 74.2%; Pred. No. 1.8e-78; tive 18; Mismatches 28; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 67.6%; Score 837; DB 4; Length 261; Best Local Similarity 75.1%; Pred. No. 1.5e-72; Matches 163; Conservative 16; Mismatches 24; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
STRAIN=20227226, PubMed=10766159;
Perletti G. Concari P., Giardini R., Marras B., Piccinini F.,
Polkman J., Chen L.;
"Antitumor activity of endostatin against carcinogen-induced rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 ETWRIEAPAATGOASSLLAGRLLEQEAASCRHAFVVLCIENSVMISFSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF282883; AAM52249.1; -SEQUENCE 261 AA; 26745 MW; CA60C920AF3E90E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 AA; 25350 MW; 38B83C0486C0E949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 23, Last annotation update)
Multi-functional protein MFP.
Homo saplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                   primary mammary tumors.";
Cancer Res. 60:1793-1796(2000).
EMBL, AF189709; AAF000975.1;
HSSP, P39061; IKOA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 74.2%
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
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Mon Mar 29 17:32:20 200

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P39061; 1KOE
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TISSUE=Liver;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=88411346; PubMed=9738008;
Halfter W., Dong S., Schurer B., Cole G.J.;
"Collagen XVIII is a basement membrane heparan sulfate proteoglycan.";
J. Biol. Chem. 273:25404-25412(1998).
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Collagen XVIII precursor.
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                        OBWXIS PRELIMINARY; PRT; 187 AA.
OBWXIS.
01-WAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (Human).
Homo sapiens (Human).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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Halfer W., Dong S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF083440; AAC33294.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 187 AA; 20448 MW; 72B1047D85838CD3 CRC64;
                                                       223 ATGQASSLLGGRLLGQSAASCHAYIVLCIENSFMTA 259
191 ATGOASSILAGRILEQEAASCRHAFVVICIENSVMTS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
67.4%; Score 835; DB 4;
Best Local Similarity 85.1%; Pred. No. 1.6e-72;
Matches 154; Conservative 14; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sheng Wu Gong Cheng Xue Bao 17:278-282(2001).
EMBL, AF416592; AAL37720.1; -.
NON TER
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NCBI_TaxID=9031;
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                                                                                                                                                                                                                             RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jia J.D., Bauer M., Eberspaecher U., Donner P., Schuppan D.; "Partial 3'-terminal cDNA sequence of rat collagen XVIII/endostatin."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jia J.D., Bauer M., Sedlaczek N., Ruehl M., Riecken B.O., Schuppan D., "Temporospatial expression of collagen XVIII/endostatin in acute and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PWRADDILAGPPRLLDPQPYPGAPHH----GSYVHFQPARPTGGPVHTHTHTHQDFQLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 HLVALNSPOPGGMRGIRGADFOCFOOARAGLAGIFRAFLSSRLODLYSIVRRADRIGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10i16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 IDSYCETWRIEAPAAIGQASSLLAGRILEQEAASCRHAFVVLCIENSVMISFSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.9%; Score 792; DB 13; Length 1344; Best Local Similarity 66.2%; Pred. No. 2.7e-67; Matches 155; Conservative 20; Mismatches 47; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.9%; Score 754; DB 11; Length 171; Best Local Similarity 81.9%; Pred, No. 9.1e-65; Matches 140; Conservative 16; Mismatches 15; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL 1 26 POTENTIAL.
SEQUENCE 1344 AA; 137402 MW; 7AA366E4FE940CCD CRC64;
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Submitted (FEE-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ236613; CA844263.1; -.
HSSP; P39061; IXOE.
NOW TER 1 1
NON TER 171
SEQUENCE 171 AA; 18933 MW; 81BE2EE3FC2C9E72 CRC64;
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR008161; Clq helix.
InterPro; IPR008160; Collagen.
InterPro; IPR001691; Conalike_lec_gl.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
Fram; FF01210; Collagen; 8.
Fram; FF0210; TSPN; 1.
ProDom; PD000007; Clg_helix; 2.
SWART; SM00210; TSPN; 1.
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171 AA; 16933 MW; 81BEZEE3FC2C6B72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
collagen type XVIII, alpha (I) chain (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. SEQUENCE FROM N.A.

P. SEQUENCE FROM N.A.

P. SEQUENCE FROM N.A.

Indentification and characterization of geneses expressed selectively in "dentification and characterization of geneses.";

The regenerating tail of Knoppus laevis tadpole.";

S. Mad 1066; BAB84674.1;

S. Mad 1066; BAB84674.1;

R. GO: GO: 0005198; F:structural molecule activity; IEA.

GO: GO: 0007155; P:cell adhesion; IEA.

R. GO: GO: 0007155; P:cell adhesion; IEA.

R. InterPro; IPR008161; Collagen.

R. InterPro; IPR013129; TSPN.

R. FORD: Collagen.

R. PFGN: PFCN: Collagen; 7.

P. Pfam; PF01391; Collagen; 7.

P. Pfam; PF01391; TSPN: 1.

PRODOUGY; Cld_helix; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSPOPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNL 120
                                                                                         61 VPIVNLKDEVLSPSWDTLFSGSQGQLHSGARIFSFDGRDVLRHPAWPQKSVWHGSDPSGR 120
                                                                 174
                                       9
                                   1 VLHLVALNTPLSGGMGTRGTRGADFQCFQQARAVGLSGTFRAFLSSRLQDLYSIVRRADRSS
                                                                   VPVVNLRDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGR
                VIHIVALNS POPGGMRGIRGAD FOCFOOARAAGLAGTFRAFISSRLODLYSIVRRADRIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PWRADDILAGPPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Gaps
                                                                                                                                                                                                                                                01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Type XVIII collagen alphal chain.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachla; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 RLIDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVM 225
                                                                                                                                        181 CETWRIEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMISFSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.4%; Score 736.5; DB 13; Length 1315; 62.6%; Pred. No. 6e-62; ive 24; Mismatches 55; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1315 AA; 134946 MW; 0C56C235DE058365 CRC64;
                                                                                                                                                                                                                        PRT; 1315 AA
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                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collagen.
SEQUENCE
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                 55
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QBJFF7
ID QBJF;
AC QBJF;
DT 01-00
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Q8QHL9
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1 PWRADDILAGPPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDFQLVLHLVA

58.9%; Score 730; DB 13; Length 1307; 63.0%; Pred. No. 2.5e-61; tive 24; Mismatches 49; Indels 12;

Matches 145; Conservative

Local Similarity

1307 AA; 134153 MW; D53EDBFE3DE34976 CRC64;

SEQUENCE Query Match

Clause H., Peterson J., Laurenter, J., Destree O., Clause H., Peterson J., Enlandeni T., Destree O., Claning of three variants of type XVIII collagen and their expression petterns during Xenopus laevis development.";

Mech. Dev. 114:109-113(2002).

EMBL, AV052763; AAL14257.1;

GO, GO:0005158; P:ctll adhesion; IEA.

GO, GO:0005159; P:cell adhesion; IEA.

InterPro; IPR003129; TSPN.

Ffan; PF01391; Collagen; 6.

Pfan; PF01391; Collagen; 6.

Pfan; PF01391; TSPN; 1.

Type XVIII collagen short variant.
Xenopus laevis (African clawed frog).
Kenopus laevis (African clawed frog).
Ambaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.

SEQUENCE FROM N.A. MEDLINE=22166979; PubMed=12175494;

NCBI_TaxID=8355;

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

9

Gaps

61 INSPOPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNL 120

1138 LNAPISGSMKSIRGVDFQCFEQARKAGLHGTFRAFLSSRLQDLYSIVRRADRQSVQIVNL 121 RDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDFSGRRLTDSY

1197

1257

181 CETWRIEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMTSFSK

180

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MEDLINE=C57BL/GJ; TISSUE=Embryo; MEDLINE=21085660; PubMed=11217851; MEDLINE=21085660; PubMed=11217851; Medline=21085660; PubMed=11217851; Medline=21085660; PubMed=11217851; Medline=21085660; PubMed=11217851; Medline=21085660; Medline=21085660; Medline=21085660; Medline=21085660; Medline=2108660; Medline=2108660; Medline=2108660; Medline=2108660; Medline=2108660; Medline=2108660; Medline=2108660; Medline=2108660; Medline=2108660; Medline=210860; Medline=2108660; Medline=210860;   Medl
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Procollagen, type XVIII, alpha 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Q9CRT2
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Created) Last sequence update)

(TrEMBLrel. 22, (TrEMBLrel. 22,

Q8JFF7; 01-OCT-2002 01-OCT-2002

PRELIMINARY;

Q8JFF7

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71 GIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNLRDEVLFPSWE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 ALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSYCETWRTEAPA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SLFSGSGGLQPGARIFSFDGRDVLRHPAWPQKSVWHGSDPSGRRLMESYCETWRIETTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 PPYTDNRYTDPVEPNIRYPVQPERNP---ITPARRPIPPVNQPGGHAHTHTSGP---GLH 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GIRGADFOCFQQARAVGLSGTFRAFLSSRLQDLYSIVRRADRGSVPIVNLXDBVLSPSWD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 LVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRIGVPV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 VNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 PP----RILDP-QP----YPGAPHHGSYVHFQPARPTGGPV----HTHTHTHQDFQLVLH 57
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Borns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Indela 19; Gaps
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haftek Z., Morran-Dubois G., Thisse B., Garrone R., Le Guellec D., Sequence and embryonic expression of collagen XVIII NC11 domain ("Sequence and the zebrafish.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ494837; CAD38825.1;
                                                                                                                                        Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                  58.6%; Score 726; DB 11; Length 160; 83.8%; Pred. No. 4.2e-62; tive 16; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                         SEQUENCE 160 AA; 17725 MW; 60F853D777C375D2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 ATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMTSFSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ATGQASSLLSGRLLEQKAASCHNSYIVLCIENSFMTSFSK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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GG; GO:0005604; C:basement membrane; IDA.
GG; GO:0001525; P:angiogenesis; IMP.
NON_TER
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                                                                                                                                                                                 Nature 409:685-690(2001).
EMBL; AK014292; BAB29249.1; -.
HSSP; P39061; IKOE.
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Matches 134; Conservative
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NCBI TaxID=7955;
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QBAWC6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1268 SIFSGDGGQFNTHIPIYSFDGRDVMTDPSWPQKVVWHGSNPHGVRLVDKYCEAWRTTDMA 1327
249 VNLKDQVLFSSWESLFSDSESRMKDNAPIYSFDGRDVLRDSAWPEKMIWHGSDGRGHRQT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 GIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNLRDEVLFPSWE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 ALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSYCETWRTEAPA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning of mouse type XV collagen sequences and mapping of the corresponding gene to 4B1-3. Comparison of mouse and human alpha 1 (XV) collagen sequences indicates divergence in the number of small collagenous domains."; Genomics 45:31-41(1997).
                                                                       178 DSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMTSFSK 230
                                                                                                            309 DNYCETWRAGDRAVIGLASSLQAGQLLQQTSSSCSSSY1ALCIENSYMTQSKK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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51.4%; Pred. No. 3.9e-45;
tive 26; Mismatches 60; Indels 21;
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GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005155; P:cell adhesion; IEA.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Collagen.
InterPro; IPR0083129; Collagen.
InterPro; IPR003129; Laminin_G.
InterPro; IPR003129; TSPN.
Pfam; PF0210; TSPN; 1.
Pram; PF02210; TSPN; 1.
Pram; PR00282; Lamid; 1.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97480713; PubMed=9338358;
Hagg P.M., Horelli-Kuitunen N., Eklund L., Palotie A.,
Pihlajaniemi T.;
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                                                                                                                                                                                                                                                                                                                                                                      01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                  PRT; 1367 AA.
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Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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Type XV collagen.
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Pihlajaniemi T.; "Cloning of mouse type XV collagen sequences and mapping of the "Cloning of mouse type XV collagen sequences and human alpha 1 (XV) collagen sequences indicates divergence in the number of small collagenous domains.";
                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 45.3%; Score 561.5; DB 11; Length 1367; Best Local Similarity 51.4%; Pred. No. 4.8e-45; Matches 113; Conservative 26; Mismatches 60; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1367 AA; 140454 MW; 40F259A3CD47C982 CRC64;
                                                                                 STRAIN=129/Sv;
MEDLINE=97480713; PubMed=9339358;
Hagg P.M., Horelli-Kuitunen N., Eklund L., Palotie A.,
         Last sequence update)
Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom, PD000007; Clg_helix; 1.
SMART; SM00282; LamG; 1.
SMART; SM00210; TSPN; 1.
                                                                                                                                            Genomics 45:31-41(1997).
                                    Mus musculus (Mouse)
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                         SEQUENCE FROM N.A.
                     Type XV collagen.
COL15A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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11 PPRLLDPQPYPGAPHHGSYVHFQPARPTGGPVHTHTHTHQDPQLVLHLVALNSPQPGGMR 70

21; Gaps

Job time : 45.5556 secs

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RESULT 15

QUESCES

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O1-UNN-2003 (TrEMBLrel. 24, Created)

DT

O1-UNN-2003 (TrEMBLrel. 24, Last sequence update)

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O1-UNN-2003 (TrEMBLrel. 25, Last annotation update)

DT

O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

COLAGEN XVIII homologue.

GN

CI-COLLAGEN XVIII homologue.

OC

ENARTYCHEN METAZOA; CHORDATA; Urochordata; Ascidiacea; Enterogona;

OC

NOSI TAXID=7719;

RP

Hotcha K., Takahashi H., Satoh N.;

RP

EMBL; AB076899; BAC5751.1;

DR

INTERPRO: IPRO0159; Pentaxin.

DR

PFam; PF01391; COllagen; 8.

DR

PFam; PF01391; COllagen; 8.

DR

PROSITE; PS00289; PENTAXIN; 1.
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Query Match 36.9%; Score 457.5; DB 5; Length 950;
Best Local Similarity 55.2%; Pred. No. 3.3e-35;
Matches 96; Conservative 17; Mismatches 60; Indels 1; Gaps 1;
Qy 53 QLVLHLVALNSPQPGGWRGIRGADFQCPQQARAAGLAGTFRAFLSSRLQDLYSIVRADR 112

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173 GRRITDSYCETWRTEAPAATGQASSLIAGRLIEQEAASCRHAFVVLCIENSVWT 226

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Search completed: March 26, 2004, 13:37:58

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

TOTE WAT 42 LY:56:41 4004

March 29, 2004, 09:11:19; Search time 2233.23 Seconds (without alignments) 10771.549 Million cell updates/sec US-09-938-391-3 555 1 cacacccaccaggacttcca......tgacctccttctccaagtag 555 6940544 Total number of hits satisfying chosen parameters: 3470272 seqs, 21671516995 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 em_sts:*
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em_pu:* GenEmbl:* Title: Perfect score: Sequence: Scoring table: Database : Searched: Run on:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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					ALIGNMENTS					
RESULT										
LOCUS		1399631			55 b	DNA	linear	PAT	06-JUN-2002	
DEFINIT		Sequence 3	from P	Patent	EP1191					
VERSION		(399631 (399631.1	GI:21	335	410					
KEYWORDS	٠.	f am	י. מיר	(do	(5					
ORGAN	W.	fami fota;	liaris Metazo	. rs	Chordata; Craniat	Ca; V	tebrata;	Eutel	leostomi;	
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AUTHORS		ard,	M.G. and Tong, X.	Tol	ig. x. Ons for diagnosing	osing and	treating		disorders	
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PAT 17-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 GAGGCCCCCGGCCGACCGGGCAGGCGTCGTCGCTGCTGCCGGGCAGGCTGCTGGAGCAG
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(Dases 1 to 555)

Shepard, M. and Tong,X.

Method and Composition for Uragnosing and treating diseases relating to angiogenesis
Peters. JP 2003000268-A 2 07-JAN-2003;

PFIZER PRODUCTS INC.

S. Canis sp. (dog)
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Method and composition for diagnosing and treating diseases
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                                                                                                                                                                   Length 555;
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Pred. No. 1.2e-64;
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/organism="Canis familiaris"
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                                                                                                                                                           Query Match
100.0%; Score 555; Di
Best Local Similarity 100.0%; Pred. No. 1.2v
Matches 555; Conservative 0; Mismatches
Patent: EP 1191036-A 3 27-MAR-2002;
Pfizer Products Inc. (US)
Location/Qualifiers
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PN JP 2003000268-A/2
PD 07-JAN-2003
PF 24-AUG-2000 US 60/227924
PR 25-AUG-2000 US 60/227924
PP MCHAEL GEORGE SHEPPARD,XTAO TONG
PC C12N15/09,A01867/027,A61813/7088,A61835/76,A61839/395 PC
A61829/395,A61846/00,A61P9/00,A61P9/10,A61P9/10,A61P17/00, PC
A61P17/02,
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A61P17/02,A61P19/02,A61P35/00,A61P35/02,A61P37/06,A61P43/00,PC
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/organism='Canis sp. (dog)'.

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source FEATURES

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                                                                                         100.0%; Score 555; DB 6;
100.0%; Pred. No. 1.2e-64;
Ative 0; Mismatches 0;
/organism="Canis sp."
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                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
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                   linear
                   DNA
                                                                                                                                                                                                                                      1. .829
/organism="Canis familiaris"
/mol_type="unassigned DNA"
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                                                                                                                                                                            involving angiogenesis
Patent: EP 1191036-A 1 27-MAR-2002;
Pfizer Products Inc. (US)
                 Ax399629 829 bp Sequence 1 from Patent EP1191036.
                                                                                                                                                                                                                       Location/Qualifiers
                                            AX399629
AX399629.1 GI:21335409
                                                                                 Canis familiaris (dog)
Canis familiaris
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Best Local Similarity 100.
Matches 555; Conservative
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AX399629
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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BD188110 829 bp DNA linear PAT 17-JUL-2003 Method and composition for diagnosing and treating diseases relating to angiogenesis.

LOCUS

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Canis Sp. (dog)

PN JP 200200266-A/1

PN JP 200300266-A/1

PP 24-AUG-2001 JP 2001254697

PR 25-AUG-2000 JB 60/227924

PR 25-AUG-2000 JB 60/227924

PI MICHAEL GEORGE SHEPARD, XAO TONG

PC C12N15/09, A01K67/027, A61K31/7088, A61K35/76, A61R39/395 PC

A61R39/395, A61K45/00,

PC A61P17/06, A61P19/02, A61P9/10, A61P25/00, A61P27/00, PC

A61P27/02,

PC A61P27/00, A61P35/00, A61P35/02, A61P37/06, A61P27/06, PC

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//organism='Canis Sp. (dog)'.
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100.0%; Score 555; DB 6; Length 829;
Best Local Similarity 100.0%; Pred. No. 1.1e-64;
Matches 555; Conservative 0; Mismatches 0; Indels (
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/mol_type="genomic DNA"
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                                                         GI:32997849
                                                         BD188110.1 GI:329
JP 2003000268-A/1.
                                                                                                                                                       Canis sp.
                                                                                                                                                                                                            Canis sp.
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TITLE
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Qy 421 GAGGCCCGGGGGGGCACCGGGCGTCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	SULT 5 240900 CUS FINITI CESSIC RSION YWORDS	ORGANISM Canis familiaris Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. REFERENCE 1 (bases 1 to 552) AUTHORS Lo.K.M., Li.Y. and Gillies, S.D. TITLE Expression and export of angiogenesis inhibitors as immunofusins JOURNAL Patent: JP 2002523036-A 20 30-JUL-2002; COMMENT OS Canis familiaris (dog) PD 30-JUL-2002 1 00000000000000000000000000000000	FF 25-AUG-1999 UF 20UG-88435 FR 25-AUG-1998 US 60/097883 PI XIN MING LO, YUE LI, STEPHEN D GILLIES PC CIZNIS/09, A61R31/711, A61R38/00, A61R39/395, A61R48/00, A61P7/00, PC A61P35/00, PC A61P35/00, A61R37/02, PC CIZNIS/00, A61R37/02	FT CDS FT CDS FOCATURES FT CDS FEATURES 1552 Source //organism="Canis familiaris" //mol_type="genomic DNA" //db_xref="taxon:9615"	Query Match Bast Local Similarity 99.8%; Pred. No. 5e-64; Matches 551; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 CACACCACGAGACTTCCAGCTGCTGCTGGTGGCCCTGAACAGCCGCAGCCG 60 1 CACACCCACCAGGACTTCCAGCTGGTGGCTGCTGAACAGCCGCAGCCG 60 1 CACACCCACCAGGACTTCCAGCCGTGCTGGTGGCCCTGAACAGCCCGCAGCCG 60	Qy 61 GGGGCATGCGAGGCATCCGAGGAGCTTCCAGTGCTTCCAGCAGGCGCGCGC	181 GTGGCGGCCGACCGGGGGGGCCGTCGTCACCTCAGGGCGGGGGCGTTTC 181 GTGGCCGGCCGACCGGGGTGCCCGTCGTCACCTCAGGGCGCGGGGTGCTCTTC 181 GTGGCCGGCCGACCGGGGGGCCCGTCGTCACCTCAGGGGCGGGGGGGTGCTCTTC 241 CCCAGCTGGAAGCCTTATTCTCGGGCTCCGAGGCCGGGGGCCGGGGGCCGGGGCCGCGCGCG

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Contact: MGC help deak
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Tissue Procurement: ATCC

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CONTACT

Sequencing Center (NISC),

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Contact: nisc.mgcaphgril.nih.gov/

Akhter.N., Ayele.K., Beckstrom-Eternberg.S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Chanker, W., Brinkley,P., Legaspi.R.,

Maduro,Q.L., Masiello,C., Maskeri.B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsuusgeon,C., Vogt.J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov estries: IRAK Plates: 68 Row: e Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRI 08-JUL-2002
                                    301 TTCTCTTTCGACGGCAGAGATGTCCTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                301 TICTCTTTCGACGGCAGAGATGTCCTGCAGCACCCCGGCCTGGCCCCGGGAAGAGAGCGTGTGG 360
                                                                                                                                  361 CACGGCTCCGACCCCAGCGGCGCCGCCTGACCGACAGCTACTGCGAGACGTGGCGGACG 420
                                                                                                                                                                                                361 CACGGCTCCGACCCCAGCGGGCGCCGCCTGACCGACAGCTGCGAGAGGGTGGCGGAGG 420
                                                                                                                                                                                                                                                                 421 GAGGCCCCGGCGGCCACCGGCCAGCGTCGTCGCTGCTGGCGGGCAGGCTGCTGGAGCAG 480
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2637)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (02-UUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Locolors 2637 bp mRNA linear PRI 08-JUI Homo sapiens, Similar to collagen, type XVIII, alpha 1, clone BC033715
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4425380"
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Pred. No. 7e-47;
0; Mismatches 79; Indels 0;
'tissue_type="Kidney, hypernephroma"
| clone_lib="NIH_MGC_89"
|lab_host="DH10B"
                                                                                                                                                                                                                                       /codon_start=3
/product="Similar to collagen,
                                                                                                                                             'note="Vector: pCMV-SPORT6"
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O'Reilly,M.S. and Folkman,M.Judah.

Therapeutic antiangiogenic endostatin compositions
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 549)

RS Lo.K.M., 11,7. and Gillies,S.D.

Expression and export of angiogenesis inhibitors as immunofusins

LEXIGAID PHARACEUTICALS CORP

OS Homo sapiens (human)

PN JP 2002523036-A/2

PD 30-UJL-2002

PP 25-AUG-1999 UP 2000566305

PP 25-AUG-1999 UP LI,STEPHEN D GILLIES

PP 25-AUG-1999 US 60/097683

PI XIN MING LO,VUE LI,STEPHEN D GILLIES

PC C12N15/00, A61K31/711,A61K39/00,A61K39/395,A61K48/00,A61P7/00,PC A61P35/00,CO7K14/745,CO7K14/78,CO7K19/00,C12N5/10,C12P21/02,PC C12N15/00,A61K37/02

PC C12N15/00,A61K37/03

PC C12N15/00,A61K37/03

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PC C12N15/00,A61K37/03

PC C12N15/00,A6
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/mol type="genomic DNA"
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RESULT

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BD266741 Section 1920 by DNA linear PAT 17-JUL-2003 Proteins that bind angiogenesis-inhibiting proteins, compositions
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method of producing and purifying endostatin?tm protein Patent: WO 0119989-A 4 22-WAR-2001;
EntreMed, Inc. (US)
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75.3%; Score 418; DB 6;
Best Local Similarity 85.3%; Pred. No. 1.9e-46;
Matches 466; Conservative 0; Mismatches 86
       DNA
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
549 bp
Sequence 4 from Patent WO0119989.
AX100086
                                                      AX100086.1 GI:13539061
                                                                                    Homo sapiens (human)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                 481 AGTGCCGCGAGCTGCCATCACGCCTACATCGTGCTCTGCATTGAGAACAGCTTCATGACT
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Angiostatin and endostatin binding proteins and methods of Patent: Wo 0193897-A 30 13-DEC-2001;
EntreMed, Inc. (US)
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    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 30 from Patent WO0193897.
AX395662
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E. (Dases I to 552)

Macdonald, N. J. and Sim, K. L.

Proteins that bind angiogenesis-inhibiting proteins, compositions and methods of use thereof

L. Proteins that bind angiogenesis-inhibiting proteins, compositions and methods of use thereof

ENTREMED INC

OS Homo sapiens (human)

PN JP 2002532068-A 2 02-OCT-2002;

ENTREMED INC

OS HOMO sapiens (human)

PN JP 2002532068-A/2

PN JP 2002532068-A/2

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Proteins that bind angiogenesis-inhibiting proteins,
compositions and
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| /organism='Homo sapiens (human)'.
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Pred. No. 1.9e-46;
0; Mismatches 80; Indels
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD266741.1 GI:33076509 JP 2002532068-A/2.
Homo sapiens (human)
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Best Local Similarity 85.3%;
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KEYWORDS SOURCE ORGANISM DEFINITION RESULT 13 BD081407 REFERENCE AUTHORS ACCESSION JOURNAL FEATURES ORIGIN ઠ 吕 ઠે 셤 ઠ g ò 셤 ठ g PAT 09-AUG-2002 61 GECGGCATGCGCGGGGGCCGACTTCCAGTGCTTCCAGCAGCGCGGGCCGTG 120 121 GGGCTGGCGGGCCTTCCTGTCCTGCCGCGCCTGCAGGACCTGTACAGCATC 180 241 CCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGGGCACGCATC 300 361 CATGGCTCGGACCCCAACGGGCGCAGGCTGACCGAGAGCTACTGTGAGACGTGGCGGACG 420 121 GGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATC 180 181 GTGCGCCGCGCGCACCGCACCGGGGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTC 240 181 GIGGGCGGIGCCGACCGCGCAGCCGIGCCCATCGICAACCICAAGGACGAGCTGCTGTTT 240 241. CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAAGCTGAAGCCCGGGGCCCGCATC 300 301 TICTCTTTCGACGCAGAGATGTCCTGCACCCCCCCTGGCCCCGGAAGAGCGTGTGG 360 301 TICTCCTTTGACGGCAAGGACGTCCTGAGGCACCCCACCTGGCCCCAGAAGAAGGGTGTGG 360 361 CACGGCTCCGACCCCAGCGGCGCCCCCTGACCGACAGCTACTGCGAGACGTGGCGGACG 420 421 GAGGCCCCGGCGGCCACCGGGCAGGCGTCGTCGCTGCTGGCGGGCAGGCTGCTGGAGCAG 480 421 daddcrcccrcddccaccaadaccrccrcdcradaadaacrccradaadaa 480 481 GAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACC 540 Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 CACAGCCACCGCGACTTCCAGCCGGTCCTCCACTGGTTGCGCTCAACAGCCCCCTGTCA 60 1 CACACCCACCAGGACTTCCAGCTGGTGCTGCACCTGGTGGCCCTGAACAGCCCGCAGCCG 60 Anglogenesis-inhibiting peptides and proteins and methods of use Patent: WO 0230382-A 2 18-APR-2002; EntreMed, Inc. (US) Location/Qualifiers 0; Gaps Query Match 75.3%; Score 418; DB 6; Length 552; Best Local Similarity 85.3%; Pred. No. 1.9e-46; Matches 466; Conservative 0; Mismatches 80; Indele linear /mol_type="unassigned DNA" /db_xref="taxon:9606" Sequence 2 from Patent WO0230982. AX473835 1. .552 /organism="Homo sapiens" AX473835.1 GI:22208005 Sim, K.L. and Liang, H. Homo sapiens (human) 541 TCCTTC 546 541 GCCTCC 546 541 TCCTTC 546 DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE RESULT 12 AX473835 LOCUS REFERENCE AUTHORS TITLE JOURNAL FEATURES ORIGIN ઠ 음 g à В ò 엄 g à g ठे g ð a à S_C ઠે ₹ 엄

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BD081407 552 bp DNA linear PAT 27-AUG-2002 Fused protein containing angiostatin component and utilization thereof in antitumor therapy.
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Fused protein containing angiostatin component and utilization
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/mol_type="genomic DNA"
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Violand,B.N. and Harding,B.I.
Pathod of producing mouse and human endostatin
Patent: US 6653099-A 9 25-NOV-2003;
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/mol_type="genomic DNA"
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AF282883 786 bp mRNA linear PRI 14-JUN-2002
Homo sapiens multi-functional protein MFP mRNA, complete cds.
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GTRGADFOCFOQARAYGLACTFAFLSSRLODLYSTVRRADRAAVPTVNLKDELLFPS
WEALFSGSEGPLKFGARIFSPDGKDVLRHPTWPQKSVWHGSDPNGRRLFESYCETWRT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 786)
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486 AGTGCCGCGAGCTGCCATCACGCCTACATCGTGCTCTGCATTGAGAACAGCTTCATGAGT
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/mol_type="mRNA"
/db_xref="taxon:9606"
1. 786
/note="antianglogenic agent"
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595 CATGGCTCGGACCCCAACGCGCAGGCTGACCGAGAGCTACTGTGAGACGTGGCGGACG 654	421 GAGGCCCCGGCGACCGCGCACGGCGTCGTTGCTTGCTGCGGGCAGGCTGCTGGAGCAG 480	655 GAGGCTCCCTCGGCCACGGGCCTCCTCGCTGCTGGGGGGGG
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Search completed: March 29, 2004, 13:38:51 Job time : 2235.23 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:	March 29, 20	104, 09:08:09	March 29, 2004, 09:08:09 ; Search time 247.424 Seconds (without alignments) 9529.183 Million cell updates/sec
Title: Perfect score:	US-09-938-391-3 555	11-3	
Sequence:	1 cacacccac	addacttcca	1 cacaccaccaccacttccatgacctccttctccaagtag 555

3373863 seqs, 2124099041 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

6747726 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000

1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2001as:*
5: geneseqn2001as:*
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9: geneseqn2003as:* N_Geneseq_29Jan04:* 1: geneseqn1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7 418 75.3 558 6 ABA99261 Aba99261 8 418 75.3 563 2 AAA208750 Aaa208750 9 418 75.3 916 3 AAAC0977 Aaa66917 418 75.3 906 3 AAAC22025 Aba06977 1 418 75.3 968 3 AAAC22025 Aac62028 2 418 75.3 3394 2 AAA783494 Aax18379 3 418 75.3 33394 2 AAX78379	16	418	75.3	ம	4	AA166529	Human
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ALIGNMENTS

RESULT 1

Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopathy; macular degeneration; ocorneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; wocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; angiofibroma; wound granulation; coronary collateral; ecerbral; arteriovenous malformation; eserbral collateral; arteriovenous malformation; ischaemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; gynaecological; gene; ss. Canine endostatin coding sequence. BP. AAL46063 standard; cDNA; 555 19-JUL-2002 (first entry) AAL46063;

Location/Qualifiers Canis familiaris.

24-AUG-2001; 2001EP-00307224. 25-AUG-2000; 2000US-0227924P. (PFIZ) PFIZER PROD INC. Sheppard MG, EP1191036-A2. 27-MAR-2002.

Tong X;

WPI; 2002-354068/39. P-PSDB; AA017430.

An isolated nucleic acid molecule for the treatment of angiogenesis-

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The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, osler webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, hemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, necessularisation, and fractures. The present sequence is the canine endostatin coding sequence
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                                             Claim 2; Fig 4; 56pp; English.
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19-JUL-2002

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Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rheumatoid architis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; plaque neovascularisation; coronary collateral; cerebral collateral; arteriovenous malformation; corolary collateral; schemmic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosia of angiogenesis related disorders, including cancer, rheumatoid arthritis, postiasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasis, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, necessatian anteriovenous malformations, ischaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine pro-endostatin coding sequence
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related disorder, such as cancers or diabetic retinopathy, encodes an
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                                                                                                                                                                                                                                                                                                                                                   "pro-endostatin"
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endostatin protein.
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BP AAZ51309 standard; DNA; 552 AAZ51309; RESULT 3 AAZS1309 THE SECOND SECON

Canine angiogenesis inhibitor, endostatin DNA 06-JUN-2000 (first entry

Canine; immunoglobulin Pc fragment; endostatin; immunofusin; anglogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic; antipportatic; antidabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; treatment; antiarteriosclerosis; tumour; metastasis; atherosclerosis; psoriasis; rheumatoid arthritis; ocular anglogenic disease; disbetic retinopsthy; macular degeneration; wound granulation; keloid scar; gene therapy; ds.

familiaris. Canis Location/Qualifiers
1. .552
/ttag=a
/troduct = "Endostatin"
/product = "Does not include stop codon" 'partial

WO200011033-A2

98US-0097883P 99WO-US019329 25-AUG-1999; 25-AUG-1998;

(LEXI-) LEXINGEN PHARM CORP.

Gillies Li Y, Б К,

WPI; 2000-237616/20. P-PSDB; AAY70265.

Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such

The patent discloses a DNA molecule encoding a fusion protein comprising a signal sequence, an immunoglobulin Fc region, and an angiogenesis inhibitor selected from angiotatin, a plasminogen fragment activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is cused to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including hammangiomas, accusic neuromas, neurofilpromas, trachomas and pyrogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibrache neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, and excessive or abnormal stimulation of endothelial cells, intestinal cells, atherosclarosis, sclerodermal and hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a DNA encoding canine endostatin ö 180 240 120 180 9 1 CACACCCACCAGGACTTCCAGCCGGTGCTGCACCTGGTGGCCCTGAACAGCCCGGAGCCG GGGCTGGCCGGCCTTCCGGGCCTTCCTGTCGCGGCTGCAGGACCTCTACAGCATC GGGCTGGCCGGCCATCCGGGCCTTCCTGTCGTCGCGGGCTGCAGGACCTCTACAGCATC GTGCGCCGCGCGCACCGCGCTGCCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTC 1 CACACCCACCAGGACTTCCAGGTGGTGCTGCAGCCTGGTGGCCCTGAACAGCCCGCAGCCG Gaps .; 0 Query Match
99.2%; Score 550.4; DB 3; Length 552;
Best Local Similarity 99.8%; Pred. No. 1e-82;
Matches 551; Conservative 0; Mismatches 1; Indels 0 tumors and macular degeneration Sequence 552 BP; 77 A; 204 C; 190 G; 81 T; 0 U; 0 Other; Example 8; Page 58-59; 68pp; English. arthritis, rheumatoid 61 121 121 181 83 ò 셤 ò ద ઠ d ò

240 360 480 300 241 CCCAGCTGGGGGCCTTATTCTCGGGCTCCGAGGCCAGCTGAAGCCCGGGGCCCGCATC 300 TTCTCTTTCGACGGCAGAGATGTCCTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGTGG 360 420 CACGGCTCCGACCCCAGCGGGCGCCCCTGACCGACAGCTACTGCGAGAGACGTCGCGGACG 420 540 GIGCGCCGCCCGACCGCACCGGGGTGCCCGTCGAACTCAAGGGACGAGGTGCTCTTC CACGGCTCCGACCCCAGCGGGCGCCTGACCGACAGCTACTGCGAGACGTGGCGGACG GAGGCCCCGGCCGCCCACCGGCGCTCGTCGCTGCTGCCGGCCAGGCTGCTGGAGCAG GAGGCCGCGAGCCCCCCCCTCCTCGTCCTCTCCATCGAGAACAGCGTCATGACC GAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACC CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGCCAGCTGAAGCCCGGGGCCCGCATC 361 (421 421 481 181 241 301 301 361 481 g à g ò 셤 ठे g ò 셤 à d

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99US-00315689.
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                                                                                                                                                                                                                                                  541 TCCTTCTCCAAGTA
                                                                                                                                                                                                                                                                                                                                                                                          Human endostatin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-365617/31.
P-PSDB; AAY94323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200026368-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'reilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-OCT-1998;
20-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel method for the preparation of recombinant human vascular endothelial cytopolesis inhibiting factor with human igGIPC fragment molecular structure and its product application. The novel factor is derived from endostatin (using PCR to screen a human foetal kidney cell cDNA library) and human IgGIPC. The product of the invention can specifically inhibit tumour vascular endostablial proliferation and can be used for curing several tumour types. This sequence encodes a fusion construct composed of human endostatin and human IgGIPC, described in the disclosure of the invention
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                                                                                               Human, endostatin, IgG1Fc; tumour; vascular endothelial proliferation;
vascular endothelial cytopoiesis inhibiting factor; inhibitor;
fusion construct; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 cacaccacceceacriccadeceerecrocacciderrececroaccacacaccecererea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Preparation of recombinant human vascular endothelial cytopoiesis suppressor factor with human LgG1Fc fragment molecular structure and application of its product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.6%; Score 419.6; DB 6; Length 1564;
84.8%; Pred. No. 4.3e-61;
ive 0; Mismatches 84; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1564 BP; 346 A; 491 C; 436 G; 291 T; 0 U; 0 Other;
                                                                                                                                                                                                       /product= "endostatin/IgG1Fc construct"
/transl except= (pos58. .60,aa:Ala)
/transl_except= (pos:811. .816,aa:GGGGSGG)
                                                                            DNA encoding human Endostatin/IgG1Fc fusion construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 7-8 (Disclosure); 12pp; Chinese.
                                                                                                                                                                                                                                                                                                                                         (LIAO-) LIAONING WEIXING BIOLOGICAL PROD INST CO.
                                                                                                                                                                           cocation/Qualifiers
                BP
                                                                                                                                                                                                                                                                                                                    2000CN-00123347
                ABQ76740 standard; DNA; 1564
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                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-751441/82.
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                                                                                                                                            Homo sapiens
Synthetic.
                                                         03-MAR-2003
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                                    ABQ76740;
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     ABQ76740
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Novel endostatin capable of inhibiting endothelial cell proliferation and angiogenesis, useful for treating angiogenesis-dependent cancers and as birth control agents.
300
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                                                                                                                                                                                                                                              361 CACCOCTCCGACCCCAGCGGGCGCCTGACCGACAGCTACTGCGAGACGTGGCGAACG 420
                                                                                                                                                                                                                                                                                                                                                                           480
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                                                            561
                                                                                                                                                                                  621
                                                                                                                                                                                                                                                                                                           681
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                                     421 GAGGCCCCGGCCCACCGGCCACGCGTCGTCGCTGCTGGCGGCAGCTGCTGGAGCAG
   241 CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGCCCAGCTGAAGCCCGGGGCCCGCATC
                                                                                                                         TTCTCTTTCGACGGCAGAGATGTCCTGCAGCACCCCCGCCTGGCCCCCGGAAGAGCGTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; endothelial cell proliferation inhibitor; collagen XVIII; angiogenesis inhibitor; anti-tumour; cytostatic; antipsoriatic; vasotropic; determatological; ophthalmological; vulnerary; antieteriosclerotic; antidiabetic; haemostatic; contraceptive; ocular angiogenic disease; atherosclerosis; scleroderma; myocardial angiogenesis; telangiectasia; angiofibroma; wound granulation, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Endostatin protein"
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The present sequence encodes an endostatin protein which is the carboxy terminal protein of human collagen XVIII. Recombinant mouse endostatin (20 mg/kg) was administered subcutaneously to mice implanted with Lewis (10 mg/kg) was administered subcutaneously to mice implanted with Lewis care in a carcinomas. There was tumour mass regression non-detectable levels after 12 days of therapy due to the angiogenesis inhibitory activity of endostatin. Thus the protein is useful for treatment of angiogenesis.

CC endostatin are useful for treating and diagnosis of tumours, ocular protein are useful for treating and diagnosis of tumours, ocular plaque neovascularisation, telanglectasia, haemophiliac joints, angiogenic diseases, osler-Webber Syndrome, myocardial angiogenesis, cangiofibroma and wound granulation of endothelial cells e.g. intestinal adhesions, atherosclerosis, scleroderma. The protein may also be useful case a birth control agent by reducing or preventing uterine vascularisation. The gene for endostatin may be isolated from cells, by the name of the mRNA using reverse transcriptase and then amplifying the man anglifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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10-AUG-1999 (first entry)
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                                          Homo sapiens.
                                                                     20-NOV-1998;
                                                                              20-NOV-1997;
                                                  WO9926480-A1
                                                            03-JUN-1999.
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Claim 10; Page 39; 68pp; English.
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AAX77719 standard; DNA; 549 BP.

ద ò g AAX77719;

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This invention describes a novel viral gene therapy vector comprising a nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine and soft and angiogenesis-inhibiting fusions and fragments, where the viral vector is sufficiently attenuated for use in human gene therapy. The products of the invention activity. The vector is used in gene therapy for inhibiting tumour growth in humans harbouring a solid tumour. The vector expresses an anti-angiogenic polypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis in the victinity of the retina. The vector is administered to cells exvivo and then administered to the patient

    GGCGGCATGCGGGGCTGCCGGGCCGACTTCCAGTGCTTCCAGCAGGCGCGGCCGTG 120

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                                                                                     Plasminogen; human; angiostatin; endostatin; gene therapy; vector; anti-angiogenic; attenuation; cytostatic; anti-diabetic; ophthalmology; tumour growth; solid tumour; diabetic retinopathy; retina; ss.
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Human endostatin DNA coding region fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-) GENETIX PHARM INC.
(MASI ) MASSACHUSETTS INST TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-angiogenic gene therapy vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 74; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US024950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses a DNA molecule encoding a fusion protein comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immunoglobulin gamma Pc fragment; endostatin; immunofusin; angiogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic; antiporiatic; antidiabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; treatment; artiarteriosclerosis; tumour; metastasis; atherosclerosis; psoriasis; rheumatoid arthritis; cullar angiogenic disease; diabetic retinopathy; macular degeneration; wound granulation; keloid scar; gene therapy; ss.
CACGGCTCCGACCCCAGCGGCGCCCTGACCGACAGCTACTGCGAGACGTGGCGGACG
                                                                                                                                                                                                  GAGGCTCCCTCGGCCACGGGCCAGGCCTCCTCGCTGCTGGGGGGGCAGGCTCCTGGGGCAG
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/note= "Does not include stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human angiogenesis inhibitor, endostatin cDNA
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by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours tumour metastasis, benign tumours including conditions tumour metastasis, benign tumours including the harmonic managed accessite neuromas, neurofibromas and pyrogenic granulomas, rheumatoid arthritis, peoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular quatoma, retrolental ibroplasia, rubeosis and Osler-Webber syndrome; myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints or night granulation, and excessive or abnormal stimulation of endothelial cells, intestinal cells, atherosclerosis, sclerodermal and hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in the construction of immunofusin containing human endostatin used in the construction of immunofusin containing human endostatin gamma acid sequence of plasminogen fragment, however, the rest of the specification refers to this sequence as being nucleotide sequence of human endostatin
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Pred. No. 8.9e-61;
0; Mismatches 80; Indels
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cocation/Qualifiers standard; DNA; 549 BP 14-SEP-2000; 2000WO-US025166 99US-0153698P 1. .540 /*tag= a 04-JUL-2001 (first entry) *tag= b /partial /partial 'partial .543 (ENTR-) ENTREMED INC 546 GCCTCC 546 TCCTTC WO200119989-A2 14-SEP-1999; Homo sapiens 481 (541 541 AAS00867 AAS00867; Key CDS CDS RESULT q ò d ઠે ô 120 120 180 180 240 240 300 300 360 360 420 420 480 480 The present sequence encodes an angiogenesis inhibiting factor (I), designated IAF-1. The present invention also describes: (1) preparation of (1) and its derivative; (2) an IAF binding acceptor and its preparation; and (3) an IAF antibody. (I) is useful for preparing new biological preparations for effectively treating various tumours and abnormal-vessel diseases. The IAF antibody is preferably a polyclonal antibody, mosaic antibody, single stranded antibody and human originated 9 Angiogenesis inhibiting factor 1 and its derivative useful for treating 1 CACACCCACCAGGACTTCCAGCTGGTGCTGCACCTGGTGGCCCTGAACAGCCCGCAGCCG CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCCGGGGCCCGCATC cciadoridesakosororieriroridadestroriadesirosecitadadescondesiones TTCTCTTTCGACGGCAGAGATGTCCTGCAGCACCCCGGCCTGGCCCCGGGAGGCGTGTGG trerectricalescalasacirectasaseaciaeceaeciaseceaeciaseaceasas CACGGCTCCGACCGCGCGCGCCTGACCGACAGCTACTGCGAGACGTGCGAACG GAGGCCCCGGGCCACCGGGCAGGCGTCGCTGCTGGCGGGGCAGGCTGCTGGAGCAG GGGCTGGCCGGCCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATC | descrete de de la contracta del la contracta de la contracta de la contracta de la contracta GTGCGCCGCCGACCGCACCGGGGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTC eecescarecessaricescesesceacratrocasiscratecasecaseceses Gaps Human, anglogenesis inhibiting factor 1; IAF-1; tumour; antibody; abnormal vessel disease; ss. . 0 75.3%; Score 418; DB 3; Length 549; llarity 85.3%; Pred. No. 8.9e-61; Conservative 0; Mismatches 80; Indels Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 U; 0 Other; Human angiogenesis inhibiting factor 1 encoding cDNA (ONCO-) INST ONCOLOGY UNDER TUMOR HOSPITAL CHINE Example 1; Fig 5; 41pp; Chinese 98CN-00117150 98CN-00117150 WPI; 2000-388168/34. Similarity P-PSDB; AAY90771 Gno 10-AUG-1998; .0-AUG-1998; Homo sapiens 466; CN1244536-A L6-FEB-2000 241 301 361 421 61 61 121 181 181 241 301 361 121 **£21** Query Match Local Yang Z, Best Loca Matches q 8 8 9 6 쇰 ò g ò g 8 ∂

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Pichia pastoris harbouring an expression plasmid
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                              481 AGTGCCGCGAGCTGCCATCACCCTACATCGTGCTCTGCATTGAGAACAGCTTCATGACT
GAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACC
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l, Schrimsher JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene fragment encoding Endostatin(TM) protein.
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Bermejo LL, Mistry FR, Shepard SR,
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The sequence encodes Human Endostatin(TM). The new method of the invention is useful for producing, recovering and purifying Endostatin (TW) from biological sources, such as biological fulles, issues, cells, culture media, and fermentation media. Endostatin(TM) is useful for treating anglogenesis mediated diseases such as solid tumours, blood treating anglogenesis mediated diseases benign tumours, blood borne tumours, leukaemias, tumour metastases, benign tumours, blood constitution is neurofibromas, rachomas, and pyogenic granulomas, rheumatoid arthritis, psoriaais, centar anglogenic diseases, of diabetic retinopathy, retinopathy of prematurity, macular of granulomas, rheumatoid arthritis, psoriaais, coular anglogenic diseases, of e.g., diabetic retinopathy, retinopathy of psecuriar glaucoma, colon cancer, retrolental fibroplasia, rubbosis, Osler-Webber Syndrome, myocardial anglogenesis, plaque neovascularisation, telangiectasia, myocardial anglogenesis, plaque neovascularisation, telangiectasia, con a subobhiliac joines, anglofibroma, and wound granulation. Endostatin(TW) is also useful for treating disease of excessive or abnormal stimulation of endothelial cells such as intestinal adhesions, atherosclerosia, colon is also subjected to lyophilisation, while preserving biological activity. Centrifugation of broth from fermentation steps in production is avoided, colon additional proteins, plaments, enzymes and other cellular cellular said and other cellular cellular said and other cellular said other cellular said other cellular said of the cellular said of the cellular said of the cellular said other cellular said other cellular said other cellular said other cellular said other cellular said other cellular said other cellular said other cellular sa Producing Endostatin protein for treating angiogenesis mediated diseases such as solid tumors, comprises recombinantly producing the protein using an expression system, and recovering and purifying the protein. WPI; 2001-244802/25. P-PSDB; AAU00896, AAU00897, AAU00898, AAU00899. Claim 6; Page 29; 67pp; English

Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 U; 0 Other;

60 Gaps ; 0 h Similarity 85.3%; Score 418; DB 5; Length 549; Similarity 85.3%; Pred. No. 8.9e-61; 66; Conservative 0; Mismatches 80; Indels 466; Conservative Query Match Local Best Loca Matches

1 CACACCCACCAGGACTTCCAGCTGGTGCTGGTGGTGGCCCTGAACAGCCCGCAGCCG 1 cacadecacedecacentecacedendenceacendentecacencaacacedecentra 61 8 유 ò

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GAGGCCCCGGCGGCCACCGGGCAGGCGTCGTCGCTGGCGGGCAGGCTGCTGGAGCAG

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Gene; human; plasminogen; angiostatin; neovascularisation; kringle domain; cell proliferation; viral vector; replication-defective; cancer; tumour; ss. New recombinant viral vector expressing human angiostatin useful for inhibiting angiogenesis in a mammalian subject with cancer or tumor. Mendez M; Chang B, Wu WW, Macarthur J, Patel S, Jooss K, Location/Qualifiers
1. .549
/*tag= a
/product= "Endostatin" Human endostatin coding sequence. ABA00774 standard; cDNA; 549 BP. 30-APR-2001; 2001US-0287673P. 05-APR-2002; 2002US-0370634P. 29-APR-2002; 2002WO-US013461 (first entry) (CELL-) CELL GENESYS INC. WPI; 2003-129131/12. P-PSDB; AAG79753. WO200288173-A2 Homo sapiens. 18-MAR-2003 07-NOV-2002 ABA00774;

This sequence encodes endostatin. Endostatin is a 20 kD C-terminal fragment of collagen XVIII that inhibits angiogenesis. The endostatin coding sequence may be used in the recombinant viral vector of the invention for obtaining angiostatin activity. The vector comprises a promoter capable of expressing human angiostatin operably linked to a structural gene encoding one or more domains of human angiostatin. The ector, which may be a replication-defective viral vector, is useful for inhibiting angiogenesis in a mammal, especially with cancer or a tumour. Note: This sequence is given incorrectly in the sequence listing of the specification as an amino acid sequence Example 4; Page 80-82; 83pp; English.

Length 549; 75.3%; Score 418; DB 7; Length 549 85.3%; Pred. No. 8.9e-61; tive 0; Mismatches 80; Indels Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 U; 0 Other; Similarity Query Match Best Local S

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combinations of angiostatin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breact, ovarian, protected, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphomal in a patient and for inhibiting tumor growth. The present sequence is used in the course of the invention
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Pest Local Similarity 85.3%; Pred. No. 8.8e-61;
Matches 466; Conservative 0; Mismatches 80;
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New angiogenesis-inhibiting protein receptors, useful in methods for treating diseases and processes that are mediated by angiogenesis, such as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.
psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease; cerebral collateral; arteriovenous malformation; rubeosis; cancer; diabetic retinopathy; arthritis; wound healing; peptic ulcer. Helicobacter related disease; fracture; cat scratch fever; ss.
                                                                                                                                                                                                                                       Disclosure; Page 86; 100pp; English
                                                                                                       99WO-US028897
                                                                                                                          98US-00206059
                                                                                                                                            (ENTR-) ENTREMED INC.
                                                                                                                                                                                WPI; 2000-412290/35.
                                                                   WO200032631-A2.
                                                                                                                                                               Macdonald NJ,
                                                                                                                          04-DEC-1998;
                                                                                     08-JUN-2000
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This invention relates to angiogenesis-inhibiting protein receptors, and the DNA sequences encoding them. Angiogenesis is the generation of new blood vessels into a tissue, and normally occurs in wound healing, foetal and embryonal development and the formation of the corpus luteum, endometrium and placenta. Angiostatin is a protein (see AAB16450 and AAA68202) involved in angiogenesis, and has an amino acid sequence similar to that of a plasminogen fragment (see murine plasminogen fragment (see MAB16451 and AAB1640). Angiostatin has the ability to inhibit angiogenesis. AAA68203). Sequences AAA66422 and AAB16522 represent coding and protein cand some of the peptides AAB16422 and AAB16522 represent coding and protein, and some of the peptides of the invention share homology with regions of laminin. Peptides AAB16422 = B16521 (excluding AAB16490) are the canding sprotein receptor fragments of the invention. The peptides bind either angiostatin or endostatin and can be used in methods for treating diseases and processes that are mediated by angiogenesis, creating diseases and processes that are mediated by angiogenesis, cuch as solid tumours, psoriasis, soleroderma, mycocardial angiogenesis, telicopater relinopathy, arthritis, wound healing, peptic ulcers, Helicobacter related diseases, fractures, placentation and cat scratch fever. They are useful for the detection and prognosis of cancer. DNA sequences A628204-A628241 encode the peptides of the invention

Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 U; 0 Other;

egectecceccacciticcedecciticcicicececciecageaccitatacacatc 180 121 dederidadesdedererereses etterialisteres etterialistikka 180 241 CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGCCCAGCTGAAGCCCGGGGCCCGCATC 300 9 1 CACACCCACCAGGACTTCCAGCTGGTGCTGCTGGTGGCCCTGAACAGCCCGCAGCCG CACAGCCACCGCGACTTCCAGCCGCTGCTCCACCTGGTTGCGCTCAACAGCCCCCTGTCA Gaps ; Query Match
Best Local Similarity 85.3%; Pred. No. 8.8e-61;
Matches 466; Conservative 0; Mismatches 80; Indels 61 61 181 121 à ф ठे a ò a ò 8 8

The present sequence encodes human endostatin. The protein is expressed in Streptomyces. Leader sequences of Streptomyces sp. strain C5 SnpA and S. venezuelae alpha-amylase proteins are linked to the N-terminal of endostatin. This ensures that endostatin protein is praduced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. The method is used for preparing soluble recombinant human, murine or primate endostatin, which is useful in the treatment of cancer, inhibition of 360 420 420 480 480 540 540 360 Preparation of soluble recombinant endostatin involves transforming Streptomycete host with expression vector comprising nucleotide sequence encoding endostatin operably linked to linker and leader peptide. TICTCCTITGACGGCAAGGACGTCCTGAGGCACCCCACCTGGCCCCAGAAGAGCGTGTGG GAGGCCCCGGGCGACCGGGCAACGGCGTCGTTGCTGGCGGGCAGCAGCAG cacegenecaaccecaecegececentaaccaaccaaccaaccaaccaaccareacce TTCTCTTTCGACGGCAGAGGATGTCCTGCAGCACCCCGGCTGGCCCCGGAAGAGGAGCGTGTGG Nucleotide sequence of human endostatin encoded by plasmid pMALCH#15. Streptomyces sp. strain C5; SnpA; S. venezuelae; alpha-amylase; endostatin; cancer; tumour growth; angiogenesis; ss. "endostatin" Location/Qualifiers 1. .552 /*tag= a /product= "endostatin Example 1; Fig 6; 57pp; English. BP. 12-APR-2000; 2000WO-US009747 AAC62023 standard; DNA; 552 06-MAR-2001 (first entry) Desanti CL, Strohl WR; (MERI) MERCK & CO INC WPI; 2000-686970/67. P-PSDB; AAB30493. 541 TCCTTC 546 541 GCCTCC 546 WO200060945-A1 13-APR-1999; Homo sapiens 19-OCT-2000 361 421 241 301 361 421 AAC62023; 301 g à 셤 à ઠ 셤 ò g 8

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tumour growth, inhibition of angiogenesis, isolation of receptors for endostatin and for identification of anti-angiogenic compounds in assays. The endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. Streptomycetes are amenable for cultivation in large fermentations allowing for large quantities of soluble endostatin to be
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                                                                                                                          Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 U; 0 Other;
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The present invention provides endostatin peptides which can be used in the modulation of angiogenesis. This is useful in the treatment of cancers, inflammation, rheumatoid arthritis, chronic articular rheumatism, psoriaels, disorders associated with inopportune invasion of prematurity, macular degeneration, conneal graft rejection, retrolental fibroplasia, rubeosis, capillary proliferation in atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent diseases include Osler-Webber syndrome, "wycardial angiogenesis, plaque neovasculisation, telangiectasia, haemophiliac joints and wound granulation. In addition, the peptides can be used as birth control
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                                                                                                                                                                                                                                                      Endostatin peptide comprising at least four endostatin amino acid residues are e.g. angiogenesis inhibitors for treating cancer and diabetic retinopathy.
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                 02-MAY-2000; 2000WO-US012063
                                                        99US-0132907P
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14-JUL-1999;
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Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 U; 0 Other;

angiogenesis-inhibiting peptides

ABK50685 standard; cDNA; 552 BP. cDNA encoding human endostatin. 13-AUG-2002 (first entry) ABK50685;

Human, angiogenesis, PITSIRE protein kinase; cancer, arthritis, macular degeneration, diabetic retinopathy; angiogenic-related disease; haemagiona, blood borne tumour; leukkaemia; neovascularisation, coronary collateral, cerbral collateral; neovascular glaucoma; corneal disease; wound healing; Helicobacter related disease; fracture; keloid; ovulation; menstruation; gene; ss.

Homo sapiens

/partial /product= "Endostatin" /note= "This sequence lacks a start codon" Location/Qualifiers ๙ 1. .552 /*tag=

WO200230982-A2

15-OCT-2001; 2001WO-US032437.

13-OCT-2000; 2000US-0240127P

(ENTR-) ENTREMED INC.

Sim KL, Liang H;

WPI; 2002-435440/46. P-PSDB; AAU97132 Regulating angiogenesis for treating scleroderma, leukemia, keloids by administering a protein that is homologous to PITSLRE protein kinase and an angiogenic factor or a protein kinase and its active fragments.

Search completed: March 29, 2004, 12:05:45

Job time : 249.424 secs

Disclosure, Fig 2B; 45pp; English.

The present invention relates to methods and compositions of inhibiting angiogenesis. The method comprises administering to a human or animal a composition comprising a protein that is homologous to PITSIRE protein. Kinases (PK) and an angiogenic factor. The method is useful for regulating angiogenic factor. The method is useful for degeneration, and diabetic retinopathy. The compositions are useful in treating diseases The method and compositions are inhibiting angiogenic related diseases. The method and compositions are useful in treating diseases and processes that are mediated by angiogenesis including haemangioms, solid tunnours, blood borne tumours, leukaemia, metastasis, telangiectasia, psoriasis, solid tumours, blood borne tumours, cunnoma, myocardial angiogenesis, Crohn's disease, plaque neovascularisation, coronary collaterals, cerebral collaterals, arteriovenous malformations, isolatemic limb angiogenesis, cornal collaterals, certolental fibroplasia, arthritis, diabetic retinopathy.

Tetrolental fibroplasia, arthritis, diabetic retinopathy actures, keloids, vasculogenesis, hemmatopoiesis, ovulation, mecular degeneration, wound healing, peptic ulcer, Helicobacter related diseases, fractures, keloids, vasculogenesis, hemmatopoiesis, ovulation, mentruation, provides a therapy for cancer that has minimal side effects.

The present sequence encodes human endostatin which is used to generate

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11日-04-426-241-2・11111

TOTE MAK 47 17.36:41 4004

OM nucleic - nucleic search, using sw model

Title: Perfect score: Sequence:

Run on:

March 29, 2004, 10:57:20 ; Search time 56.1416 Seconds (without alignments) 5486.086 Million cell updates/sec US-09-938-391-3 555 1 cacaccaaccaggacttcca......tgacctccttctccaagtag 555

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

682709 segs, 277475446 residues Searched:

1365418 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

nic Endostatin Compositions	DB 4; Length 546; .3e-74; es 80; Indels 0; Gaps 0;	ACTGGTGGCCTGAACAGCCCGCAGCCG 60		CTGTCGTCGCGGCTGCAGACCTCTACAGCATC 180	regreaccreaggacgaggrerrre 240	IGGGCCAGCTGAAGCCCGGGCCCGCATC 300 	CTCTTTCGACGGCAGAGATGTCCTGCAGCACCCGGCTGGCCCGGAAGAGCGTGTGG 360	CGACACATACTGCGACACGTGGCGGACG 420
5-689-4 No 6-346510 LINCORMATION: CLANT: FOLKman, Judah CLANT: FOLKman, Judah CLANT: O'REILLY, Michael CRANT: O'REILLY, Michael CRANT: APPLICATION NUMBER: US/09/315,689 NY PILING DATE: 1999-05-20 NY FILING DATE: 1999-05-20 NY SEQ ID NOS: 6 NY ARE: PATENTIN VET: 2.0 NO 4 TH: 546 NY MINGN: HOMO SAPIENS SEG 9-4	ch 75.3%; Score 418; D. Similarity 85.3%; Pred. No. 1.3 466; Conservative 0; Mismatches	1 CACACCCACCAGGACTICCAGCTGGTGCACCTGGTGGCCCTGAACAGCCCGCAGCCG	61 GGCGGCATGCGAGGCATCCGGGGAGCGGACTTCCAGTGCTTCCAGCAGGCGCGCGC	GGGCTGGCGGCACCTTCCGGGCCTTC GGGCTGGCGGCACCTTCCGGGCCTTC	181 GIGCGCCGCCGACCGCACCGGGGTCCCCGTCGTCAACCTCAGGACGACGAGGTGCTCTTC	241 CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATC 	301 TTCTCTTTCGACGCAGGAGATGTCCTGCAG 	361 CACGGCTCCGACCCCAGGGGGCGCCCTGACCGACAGCTACTGCGAGACGTGGCGAACG
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481 GAGGCCGCGAGCTGCCGCCACGCCTTCGTGCTCTGCATCGAGAACAGCGTCATGACC 540
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Sequence 30, Application US/09206059

Patent No. 6201104

GENERAL INFORMATION:
APPLICANT: MacDonald, Nicholas
APPLICANT: Sim, Kim Lee
APPLICANT: Sim, Kim Lee
APPLICANT: Sim, Kim Lee
APPLICANT: Sim, Kim Lee
APPLICANT: Sim, Kim Lee
APPLICANT: Sim, Kim Lee
CURRENT: PRESENCE: 05213-0370

CURRENT APPLICATION NUMBER: US/09/206,059

CURRENT FILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver. 2.0
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IENGTH: 552
TYPE: DNA
; ORGANISM: HOMO Sapiens
US-09-206-059-30
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                                                                                                                                                                                                                         APPLICANT: Harding, E.I.
APPLICANT: Harding, E.I.
APPLICANT: Violand, B.N.
TITLE OF INVENTION: Method of producing mouse and human
TITLE OF INVENTION: endostatin
FILE REFERENCE: S03071-00-US
CURRENT APPLICATION NUMBER: US/09/231,077D
CURRENT FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-02-23
NUMBER: OF SEQ ID NOS: 13
SOFTWARE: FRASESQ for Windows Version 4.0
Sequence 9, Application US/09231077D; Patent No. 6653098; GENERAL INFORMATION:
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us-09-938-391-3.rni

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1924 GAGGCTCCCTCGGCCACGGGCCAGGCCTCCTCGCTGCTGGGGGGGCCAGGCTCCTGGGGGCAG 1983
                                                                                                                                                                                                                                                                                                                                                1984 AGTGCCGGAGCTGCCATCACCTCTGCTGCTTCTGAGAACAGCTTCATGACT 2043
                                     1864 CATGGCTCGGACCCCAACGGGCGCAGGCTGACCGAGAGCTACTGTGAGACGTGGCGGACG 1923
                                                                                                                      421 GAGGCCCCGGCGGCCACCGGCCAGCGTCGTCGCTGCTGGCGGCAGGCTGCTGGAGCAG 480
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Sequence 6, Application US/09315689
Patent No. 6346510
GENERAL INFORMATION:
APPLICANT: FOLKMAN, Judah
APPLICANT: O'Reàlly, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0229
CURRENT APPLICATION NUMBER: US/09/315,689
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.6'
Matches 457; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-315-689-6
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RESULT 4

US-08-159-784-4

IS-08-159-784-4

Sequence 4, Application US/08159784

Sequence No. 5643783

GENERAL INFORMATION:

APPLICANT: Bjorn R. Olsen

TILLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF

NUMBER OF SEQUENCES: 9

CORRESPENDENCE: 9

CITY: BOSTON

STREET: 225 Franklin Street

CITY: BOSTON

STRIET: Massachusetts

CONTRY: BOSTON

STRIE Massachusetts

COMPUTER: BOSTON

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: MORGERECET (Version 5.0)

SOFTWARE: MORGERECET (Version 5.0)

SOFTWARE: December 1, 1993 'APPLICATION NUMBER: US/08/159,784

FILING DATE: December 1, 1993 'APPLICATION NUMBER: MS-DOS (WESSION 5.0)

PRIOR APPLICATION DATA:

APPLICATION NUMBER: MS-DOS (WESSION 5.0)

PRIOR APPLICATION DATA:

APPLICATION NUMBER: MS-DOS (WESSION 5.0)

FILING DATE: DECEMBER: MS-DOS (WESSION 5.0)

PRIOR APPLICATION NUMBER: MS-DOS (WESSION 5.0)

FILING DATE: MS-DOS (WESSION MIMBER: MS-DOS (WESION MIMBER: MS-DOS (WESSION MIMBE
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NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00246/170001
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3394
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Sequence 3, Application US/09449293
; Sequence 3, Application US/09449293
; Patent No. 6267954;
; Patent IN VORMATION;
APPLICANT: Abitbol, Marc
; APPLICANT: Bossard, Carine
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APPLICANT: Bonnel, Sebastien
APPLICANT: Bonnel, Sebastien
APPLICANT: Prats, Herve
APPLICANT: Prats, Herve
APPLICANT: Neumer-Vehle, Martin
APPLICANT: Honnel, Sebastien
APPLICANT: Number, Jiri
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US-09-449-293-3
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APPLICANT: Wenseche, Maurice
APPLICANT: Bossard, Carino
APPLICANT: Van Den Berghe, Loic
APPLICANT: Won Den Berghe, Loic
APPLICANT: Parts, Herve
APPLICANT: Honjer, Jii
APPLICANT: Neuner-Jehle, Martin
TITLE OF INVENTION: INTRACCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
CURRENT APPLICATION NUMBER: US/09/775,325
CURRENT FILING DATE: 2001-02-01
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PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
                                                                 Sequence 3, Application US/09775325
Patent No. 6500449
GENERAL INFORMATION:
APPLICANT: Abitbol, Marc
APPLICANT: Uteza, Yves
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US-09-775-325-3
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                                    Sequence 3, Application US/03775174

Fatent No. 6663894

GENERAL INCOMATION:
APPLICANT: Abitbol, Marc
APPLICANT: Windown Seche, Maurice
APPLICANT: Menasche, Maurice
APPLICANT: Wan Den Berghe, Loic
APPLICANT: Bonnal, Sebastian
APPLICANT: Bonnal, Sebastian
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APPLICANT: Bonnal, Sebastian
APPLICANT: Seuner-Jehle, Martin
APPLICANT: Remember-John, Martin
APPLICANT: Remember-John, Martin
APPLICANT: Remember-John, Martin
APPLICANT: Seuner-John NUMBER: US/09/775,174
CURRENT FILING DATE: 2001-02-01
PRIOR PLILING DATE: 2001-02-01
PRIOR PLILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CACACCCACCAGGACTTCCAGGTGGTGCTGCAGCTGGTGGCCCTGAACAGCCCGCAGCCG
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; ORGANISM: Rattus rattus
US-09-775-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
LENGTH: 558
RESULT 8
US-09-775-174-3
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Sequence 37, Application US/0898526
| Patent No. 6080728
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: ENCONDING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE TITLE OF INVENTION: THERAPY
| NUMBER OF SEQUENCES: 43 |
| CORRESPONDENCE ADDRESS:
| STREET: 1220 Market Street, P.O. Box 2207 |
| CITY: Wilmington | COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GIGGGCCGCGCCGACCGCACCGGGGGGCCCCGTCGACCTCAGGGACGAGGTGCTCTTC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.7%; Score 375.8; DB 3; Best Local Similarity 79.8%; Pred. No. 3e-66; Matches 443; Conservative 0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATIONED DATE: 16-UTL-1996
ATTONEDY/AGENT INFORMATION:
NAME: MGMOTTOW JT., ROBERT G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECUTION: (302) 658-21.7
TELEPAX: (302) 658-5613
TELEPAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS: LENGTH: 565 base pairs TYPE: nucleic acid STRANDEDNESS: single "noDLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
US-08-985-526-37
US-08-985-526-37
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		このでは、	481 GAGGCCGCGAGCTGCCGCCACGCCTTCGTGCTGCTGCTGCAGGACGCGCGTCGCTGCAGGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	LLL C**********************************	541 TCCTTCTCCAAGTAG	Db 551 TCTTCCCAAAIAG 565	RESULT 10	US-08-159-784-1 ; Sequence 1, Application US/08159784	A3783 RMATION:	APPLICANT: BJOIN K. OLDEN ; TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF	NOMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:	. 53	; Clif Boscou ; STAMBS A Massachusetts	; COUNTRY : U.S.A.	COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: PREADABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: WordPerfect (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/159,784 FILING DATE: December 1, 1993 CLASIPICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 230 PRIOR APPLICATION DATA: APPLICATION DATE: FILING DATE: APPLICATION NUMBER: 29,066 REFERENCE/DOCKET NUMBER: 0246/170001 TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-8906 TELEPAX: (617) 542-8906 TELEFAX: (617) 542-8906	ine	٠ <u>٢</u>	0	Oy 1 CACACCCACCAGGACTTCCAGGTGGTGCTGCTGGTGGCCCTGAACAGCCGGAGCCG 60	Db 3313 CATACTCATCAGGACTTTCAGCCAGTGCTCCACCTGGTGGGCACTGAACACCCCCTGTCT 3372	Oy 61 GGGGGATGCGAGGCATCCGGGAAGCGAACTTCCAGTGCTTCCAGCAGCGCGCGC	Db 3373 GGAGGCATGCTGGTATCCGTGGAGCAGATTCCAGTGCTTCCAGCAAGCCGAGCCGTG 3432	QY 121 GGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGCAGGACCTCTACAGCATC 180	Db 3433 GGGCTGTCGGGCACCTTCCGGGCTTTCCTGTCTCTAGGCTGCAGGATCTCTAAGCATC 3492

HIT 11
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10-561-3493 GTGCGCCCTGCTGACCGGGGGTCTGTGCCCATCGTCACCTGAAGGACGAGGTGCTATCT 3552 82 GGAGGCATGCGTGGTATCCGTGGAGCAGATTTCCAGTGCTTCCAGCAAGCCCGAGCGGTG 141 180 201 GIGGGCGCGCCGACCGCACCGGGGGGCCGGTCGTCAACCTCAGGGACGAGGTGCTTC 240 181 gracegegegegegegenecegegerecegegereseres 240 241 CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGCCCAGCTGAAGCCCGGGGCCCGCATC 300 81 1 CACACCACCAGGAGTTCCAGCTGGTGCTGCTGGTGGCCCTGAACAGCCCGCAGCCG
22 CATACTCATCAGGACTTTCAGCCAGTGCTCCACCTGGTGGCACTGAACACCCCCCTGTGT 121 gagerroccegoracerrecegacerrecerareaceaceaceaceacerecaceace 142 GGGCTGTGGGGCACCTTCCGGGCTTTCCTGTAGGCTGCAGGATCTCTATAGCATC Gaps EXTRIPORMATION: Description of Artificial Sequence: SYNTHETIC EXTREMATION: OLIGONUCLEOTIDE AFFERS: CDS (7/KEY: CDS (7/KEY: CDS (7/KEY: CDS (7/KEY))); (5/73) Match 67.3%; Score 373.4; DB 4; Length 573; ocal Similarity 79.9%; Pred. No. 8.9e-66; s 440; Conservative 0; Mismatches 111; Indels 0; i: DNA NISM: Artificial Sequence 181 7 8

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RESULT 13
US-09-561-526-12
US-09-561-526-12
Sequence 12, Application US/09561526
Patent No. 6416758
General invormation:
The patent No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No
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                                 322 TTTTCTTTTGACGGCAGAGATGTCCTGAGACACCCAGCCTGGCCGCAGAAGAGGCGTATGG 381
                                                                                                                                                                                                        CACGGCTCCGACCCCAGCGGGGGCGCCTGACCGACAGCTACTGCGAGACGTGGCGGACG 420
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CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATC
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CRGANIEM: Artificial Sequence

CRGANIEM:

OTHER INFORMATION: DIGONUCLEOTIDE

NAME/KEST: CDS

LOCATION: (1)..(573)

US-09-561-526-12
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Best Local Similarity 79.9%
Matches 440; Conservative
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Patent No. 634221
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REPERENCE: 4001.002584
CURRENT APPLICATION NUMBER: 06/131,432
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 06/131,432
PRIOR APPLICATION NUMBER: 06/131,432
SPRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 12
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  GTGCGCCGTGCTGACCGGGGGTCTGTGCCCCATCGTCAACCTGAAGGACGAGGTGCTATCT
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CTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
COTHER INFORMATION: OLIGONUCLEOTIDE
NAME/KEY: CDS
LOCATION: (1)..(573)
US-09-561-108-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.3%; Score 373.4; DB 4; Length 573; Best Local Similarity 79.9%; Pred. No. 8.9e-66; Matches 440; Conservative 0; Mismatches 111; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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TCTTTCTCCAA 572
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US-09-561-108-12
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Query Match 67.3%; Score 373.4; DB 4; Length 573;
Best Local Similarity 79.9%; Pred. No. 8.9e-66;
Matches 440; Conservative 0; Mismatches 111; Indels 0; Gaps 0;
                                                                                                                 301 IICICITICGACGCAGAGAIGICCIGCAGCACCCCGCCIGGCCCCGGAAGAGCGIGIGG 360
                                                              262 CCCAGCTGGGACTCCCTGTTTTCTGGCTCCCAGGGTCAACTGCAACCCGGGGCCCGCATC 321
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Sequence 12, Application US/09561499

Sequence No. 6524633

GENERAL INFORMATION:

APPLICANT: PHILIP E. Thorpe

APPLICANT: Rolf A. Brekken

TILLE OF INVENTION:

ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF

FILE REFERENCE: 4001.002582

CURRENT APPLICATION NUMBER: US/09/561,499

CURRENT APPLICATION NUMBER: 06/131,432

PRIOR APPLICATION NUMBER: 60/131,432

PRIOR APPLICATION NUMBER: 60/131,432

PRIOR PLING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SOOTWARE: PATENTIN Ver. 2.0

SEQ ID NO 12

LENGHAE: 573
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COTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
COTHER INFORMATION: OLIGONUCLECTIDE
NAME/KEY: CDS
LOCATION: (1)..(573)
US-09-561-499-12
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ORGANISM: Artificial Sequence
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562 TCTTTCTCCAA 572
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US-09-561-499-12
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381	420	441	480 501	540	561					*					0	09	4	N	4	180	0	4. (261	0	321	360
301 TICTITICARCACAGAGAGATGTCCTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGTGG	QY 361 CACGGCTCCGACGCGCGCGCCTGACGACAGCTACTGCGAGAGAGA		Qy 421 GAGGCCCCGGCGGCCACCGGGCACGCGCTGCTGCTGGCGGGCAGGCTGCTCGAGGCAGGC	Qy 481 GAGGCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACC		Qy 541 TCCTTCTCCAA 551	Db 562 TCTTCTCCAA 572	RESULT 15 US-09-998-831-12 ; Sequence 12, Application US/09998831 ; Patent No. 6676941 ; GENERAL INFORMATION: ; APPLICANT: Philip E. Thorpe	APPLICANT: Rolf A. Brekken TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY TITLE OF INVENTION: INHIBITING VEGF	: TLDE REFERENCE: #VOLTO-2554; CURRENT FILLIO DATE: 2001-11-30; CURRENT FILLIO DATE: 2001-11-30;	FRICK AFFILCATION NUMBER: 09/001,108 FRICK FILING DATE: 000-04-28 NUMBER OF SEQ ID NOS: 44 SOFTWARE: Patentin Ver. 2.0	; SEQ ID NO 12 ; LENGTH: 573 ; TYPE: DNA ; ORGANISM: Artificial Sequence	; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC OTHER INFORMATION: OLIGONUCLEOTIDE INVARINCEY: CDS DOCUMENT (573) US-09-988-811-12	Ouery Match 67.3%; Score 373.4; DB 4; Best Local Similarity 79.9%; Pred, No. 8.9e-66;	es 440; Conservative 0; Mismatches	1 CACACCACAGGACTTCCAGCTGGTGCTGCACCTGGTGGCCCTGAACAGCCCGCAGCCG		61 GGCGGCATGCGAGGCATCCGGGGACTTCCAGTGCTTCCAGCAGGCGCGCGC	82 GGAGGCATGCGTGGTATCCGTGGAGCAGATTTCCAGTGCTTCCAGCAAGCCCGAGCCGTG	121 GGGCTGGCCGGCACTTCCGGGCCTTCCTGTCGCGGCTGCAGGACCTCTACAGCATC	142 GGGCTGTCGGGCCACCTTCCGGGCTTTCCTGTCCTCTAGGCTGCAGGATCTCTATAGCATC	181 GIGCGCGCGCGACCGCACCGGGGGCGCCCGTCGTCAACCTCAAGGACGAGGTGCTCTTC	202 GIGCGCCGIGCTGACCGGGGGGTCTGTGCCCATCGTCAACCTGAAGGACGAGGTGCTAICI	241 CCCAGCIGGGAGGCCTIAIICICGGGCTCCGAGGGCCAGGCTGAAGCCCGGGGCCCGCATC	262 CCCAGCTGGGACTCCCTGTTTTCTGGCTCCCAGGGTCAACTGCAACCCGGGGCCCGCATC	Qy 301 TICICITICGACGGCAGAGAIGICCTGCAGCACCCCGCCTGGCCCCGGAAGACGGTGGG

Search completed: March 29, 2004, 13:41:22 Job time : 59:1416 secs

us-09-938-391-3.rnpb

Sequence 59, Appl Sequence 48, Appl Sequence 3, Appli Sequence 3, Appli Sequence 37, Appli Sequence 10, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appl Sequence 15, Appl Sequence 64, Appl Sequence 67, Appl Sequence 67, Appl Sequence 67, Appl Sequence 67, Appl Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3078, Appl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

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RESULT 1
US-09-38-191-3
; Sequence 3, Application US/09938391
; Publication No. US20030158099A1
; Foublication No. US20030158099A1
; GENERAL INFORMATION:
; APPLICAMY: TOTG, et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING
; TITLE OF INVENTION: DISORDERS INVOLVING ANGIOGENESIS
; FILE REPERENCE: POLOTO90A
; CURRENT APPLICATION NUMBER: US/09/938,391
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; TYPE: DNA
; TYPE: DNA
; ORGANISM: CANINE ENDOSTATIN NUCLECTIDE SEQUENCE
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Sequence 1, Appli
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Sequence 1, Appli
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1 cacaccaaccaggacttcca......tgacctccttctccaagtag
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 US-10-28-10-2178

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Sequence 50, Application US/10131241

Publication No. US20030012792A1

Publication No. US20030012792A1

SEQUENCE 50, Application No. US20030012792A1

APPLICANT: Fortier, Anne H.

APPLICANT: Fortier, Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Frolife

TITLE OF INVENTION: Composition and Methods for Inhibiting Endothelial Cell Frolife

TITLE OF INVENTION: OND WASER: US,10,1131,241

CURRENT FILING DATE: 1999-10-06

PRIOR PRIOR PLICATION NUMBER: US, 09/413,049

PRIOR PLICATION NUMBER: US, 09/316,802

PRIOR FILING DATE: 1999-05-21

PRIOR FILING DATE: 1999-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin Version 3.1

SEQ ID NO 50

LENGTH: 552
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                                                                                                                421 GAGGCCCCGGCGGCCACCGGGCAGGCGTCGCTGCTGCCGGGCAGGCTGCTGCAGCAG 480
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361 CACGGCTCCGACCCCAGGGGGCGCCGCTGACCGACAGCTACTGCGAGACGTGGCGGACG 420
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                                                                                                                                                                                                                                                                                                                                                                                                           TCCTTCTCCAAG 552
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Publication No. US20030139365A1

GENERAL INFORMATION:
APPLICANT: Lo, Kin-Ming
APPLICANT: Lo, Kin-Ming
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: 1 Munucfusins
FILE REFERENCE: LEX-006C1
CURRENT APPLICATION NUMBER: US/10/292,418
CURRENT FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
MARCHING TO 34
M
361 CACGGCTCCGACCCCAGCGGCGCCGCCTGACCGACAGCTACTGCGAGACGTGGCGGACG 420
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; OTHER INFORMATION: Endostatin US-10-292-418-34
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ESULT 6 S-10-13 Sequen	SULT 6 -10-131-241-53 Sequence 53, Application US/10131241	RESULT US-10-2 ; Seque ; Publi	RESULT 7 US-10-292-418-3 ; Sequence 3, Application US/10292418 ; Publication No. US20030139365A1 ; GENERAL INFORMATION:
Public GENERA APPLI	Publication No. US20030012792A1 GENERAL INFORMATION APPLICANT: HOLAGAV. John W	APPL APPL	ICANT: Lo, Kin-Ming ICANT: Li, Yue cranhan n
APPLI	APPLICANT: Fortier, Anne H. TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer TITLE OF INVENTION: compositions and Methods for Inhibiting Endothelial Cell Prolifer TITLE OF INVENTION: and Partier An	TITE ;	TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as TITLE OF INVENTION: Immunofusins
FILE	uig cancer	; file ; curr ; curr	KEKEKEKEULE, LEK-UO&CI SNY APPLICATION NUMBER: US/10/292,418 SNY FILING DATE: 2002-11-12
PRIOF PRIOF	NAT FLILIG DATE: 2002-077-22 PAPLICATION UNMER: US 09/413,049 FILING DATE: 1999-10-06	PRIO ; PRIO ; PRIO	R APPLICATION NUMBER: 09/383,315 R FILING DATE: 1999-08-25 R APPLICATION NUMBER: 13 60/097,883
PRIOF	A APPLICATION NUMBER: US 09/316,802 A FILING DATE: 1999-08-21 A PPLICATION NUMBER: US 60/086,586	, PRIO , NUMB	PRIOR FILING DATE: 1998-08-25 NUMBER OF SRO ID NOS: 54 COPPERATE TO FEAST TO 10
PRIOF	R OF SEQ ID NOS: 65		3 3 549
SEQ ID)FTWAKE: Patentin version 3.1 ENGTH: 549		TYVPE: DNA ORGANISM: Homo sapiens PEATURE:
TYPE: ORGANI S-10-131-	TYPE: DNA ORGANISM: Homo sapíens -10-131-241-53	S-1	NAME/KEY: CDS LOCATION: (1)(549) OTHER INFORMATION: endostatin 0-292-418-3
Query Match Best Local B Matches 46	Query Match 75.3%; Score 418; DB 14; Length 549; Best Local Similarity 85.3%; Pred. No. 2.1e-86; Matches 466; Conservative 0; Mismatches 80; Indels 0; Gaps 0;	Query Best	Score 418; DB 14; Length 549; Pred. No. 2.1e-86;
	1 CACACCACCAGACTTCCAGCTGGTGCTGGTGGCCTTGAACAGCCGGCAGCCG 60	Match	vative 0; Mismatches 80; Indels 0; Gaps
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US-09-880-107-2178
US-09-880-107-2178
Sequence 2178, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTYON: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTYON: Gene Expression Profiles in Liver Cancer;
TILE REFERENCE: 44921-5028-WO
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2178
LENGTH: 3394
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L22548
US-09-880-107-2178
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Best Local Similarity 85.3%; Score 418; DB 9; Length 3394;
Best Local Similarity 85.3%; Pred. No. 1.6e-86;
Matches 466; Conservative 0; Mismatches 80; Indels
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ORGANISM: Homo sapiens
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; Sequence 30, Application US/09873676
; Patent No. US200200728931
; GENERAL INFORMATION:
    APPLICANT: MacDonald, Nicholas J.
    APPLICANT: Sim, Kim, L.
    APPLICANT: Sim, L.
    APPLICANT
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Matches 466; Conservative
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ORGANISM: Homo sapiens
US-09-873-676-30
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US-09-873-676-30
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US-10-264-049-835

sequence 835, Application US/10264049

sequence 835, Application US/10264049

publication No. US20040005579A1

GENERAL INFORMATION:

APPLICANT: Bisse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA133P1

CURRENT APPLICATION NUMBER: US/10/264,049

CURRENT FILING DATE: 2002-10-04

PRIOR RILING DATE: 2002-06-07

PRIOR RILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 4360

SOUTWARE: PatentIn Ver. 3.1

SEQ ID NO 835

LIENGTH: 4875
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75.3%; Score 418; DB 15;
Best Local Similarity 85.3%; Pred. No. 1.5e-86;
Matches 466; Conservative 0; Mismatches 80;
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CORGANISM: Homo sapiens
US-10-264-049-835
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Subjection No. US20030073144A1

SUBJECTION No. Darin R.

SUBJECTION Ralos, Michael D.

SUBJECTION Persing, David H.

SUBJECTION Hepler, William T.

APPLICANT: Usang, Yuqiu H.

SUBJECTION NO. AND DIAGNOSIS OF PANCREATIC CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

CURRENT APPLICATION NUMBER: US/10/060,036

CURRENT APPLICATION NUMBER: US/10/060,036

CURRENT FILING DATE: 2002-01-30

NUMBER OF SEQ ID NOS: 4560

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 144

SEQ ID NO 144

LENGTH 4551
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75.3%; Score 418; DB 14; Length 4551;
Best Local Similarity 85.3%; Pred. No. 1.6e-86;
Matches 466; Conservative 0; Mismatches 80; Indels 0
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CORGANISM: Homo sapiens
US-10-060-036-144
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Sequence 51, Application US/10131241

Publication No. US20030012792A1

GENERAL INFORMATION:
APPLICANT: FORTIGE, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolife
TITLE OF INVENTION: and Regulating Anglogenesis Using Cancer Markers
FILE REPERENCE: 05213-0344 41770-271565
CURRENT FILING DATE: 1050-07-22
CURRENT FILING DATE: 1090-07-22

CURRENT FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-05-21

PRIOR FILING DATE: 1999-05-21

PRIOR FILING DATE: 1999-05-21

PRIOR FILING DATE: 1998-05-22

WHIGHER OF SEQ ID NOS: 65

SOFTWARE: PATENTIN VERSION 3.1

FORTIAL OF THE OFFICE OF
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Matches 523; Conservative
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                                                                                                                                                                                                                                     APPLICANT: Campochiaro, Peter A.
APPLICANT: Dixon, Katharine H.
APPLICANT: Dixon, Katharine H.
APPLICANT: Brazzell, Romulus K.
TITLE OP INVENTION: METHOD FOR TREATING OCULAR
TITLE OF INVENTION: MEDVASCULARIZATION
FILE REFERENCE: 4-31881B.
CURRENT APPLICATION NUMBER: US/10/080,797
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                      Sequence 2, Application US/10080797; Publication No. US20020183253A1; GENERAL INFORMATION:
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Best Local Similarity
Matches 465; Conserv
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              541 TCCTTC
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; TYPE: DNA
; ORGANISM: Human
US-10-080-797-2
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RESULT 13 US-10-131-241-51 us-09-938-391-3.rnpb

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WESULY 15

US=10-045

Squance 6, Application US/10042347

Fublication No. US2030114370A1

Squance 10. Willy Michael 8.

APPLICANT: O'Reilly Michael 8.

TITLE OF INVENTION: Nucleic Acid Molecules Encoding Endostatin Protein and Peptide 1

TITLE OF INVENTION: Nucleic Acid Molecules Encoding Endostatin Protein and Peptide 1

TITLE OF INVENTION: Nucleic 8.

PRIOR PELING DATE: 1999-05-10.

PRIOR PELING DATE: 1998-10-30

PRIOR PELING DATE: 1998-0-16

PRIOR PELING DATE: 1998-0-16

PRIOR PELING DATE: 1998-0-0-17

NUMBER OF SEQ ID NOS: 6

SOFTWARR: Retentin Version 3.1

SSEQ ID NO 6

LENGTH: 534
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Matches 462; Conservative
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APPLICANT: Stone, David
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APPLICANT: Labobrow, David
APPLICANT: Labobrow, David
APPLICANT: Labobrow, Denise et al.
TITLE DG INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOR
FILE REPERBRUCE: 21402-416 A
CURRENT FILING DATE: 2010-60-10
FRIOR APPLICANTON NUMBER: 60/320, 904
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o. US20040043928A1
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Ji, Weizhen
Ji, Weizhen
Padigaru, Muralidhara
Casman, Stacie
Voss, Edward
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Malyankar, Uriel
MacDougall, John
Stone, David
Alsobrook II, John
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Patturajan, Meera
Penar, Carol
Rieger, Daniel
Shimkets, Richard
Zerhusen, Bryan
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Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
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Gorman, Linda
Leite, Mario
Vernet, Corine
Anderson, David
Guo, Xiaojia
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Gerlach, Valerie
Hjalt, Tord
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Publication No. US200400439
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
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; LOCATION: (1)..(552)
US-10-210-172-161
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253 GCCTTAITCIGGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATCTTCTCTTTCGAC 312 241 GCTCTGITCTCAGGCTCTGAAGCCCGGGGCAGCATCTTCTCTTTTGAC 300
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74.0%; Score 410.8; DB 14; Length 534;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-042-347-6
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Search completed: March 29, 2004, 16:40:38 Job time : 231.15 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

MOII MAI 49 11.32.42 400

March 29, 2004, 11:07:01; Search time 1704.7 Seconds (without alignments) 9722.244 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-938-391-3 555 1 cacaccaccaggacttcca.....tgacctccttctccaagtag 555

Title: Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

55026578 Total number of hits satisfying chosen parameters:

27513289 segs, 14931090276 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database :

em_estba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

BF074459 SS1 bp mRNA linear EST 25-APR-2001 221893 MARC 2BOV Bos taurus cDNA 5', mRNA sequence. BF074459	Br0/4459.1 G1:1086/3/0 BST. Bos taurus (cow) Bos taurus Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos	1 (bases 1 to 551) Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Sankh, T.P.L., Grosse, W.M., Cho, J., Fahrenkrug, S.C., Casas, B., Wray, J.B., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Ouackenbush, J. and Keele, J. W.	Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and consetruction of a gene index for cattle canome Res. 11 (4), 656-630 (2001)	21180013 11282978	CONTACT: SMILL 1PL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
RESULT 1 BF074459 LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	MEDLINE	COMMENT

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SOURCE
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              Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: AGGAACAGCATGACGAG
BACKWARD: GTTTTCCCAGTCACGAG
Plate: 81 row: F column: 9
Seq primer: ATTTAGGTGACATARG.
                                                                                                                                                  1..551

1..551

/ Organism="Bos taurus"

/ Mol_Lype="mRNA"

/ tissue_type="pooled"

/ tab_hote="booled"

/ lab_hote="bottor: pcMV SPORT6; Site_1: NotI; Site_2: SalI;

/ lote="Vector: pcMV SPORT6; Site_1: NotI; Site_2: SalI;

/ Library made from pooled tissue from testis, thymus,

semitendonosus muscle, longissimus muscle, pancreas,

adrenal, and endometrium."
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Pred. No. 3.8e-53;
0; Mismatches 57; Indels 0;
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/clone="INAGE:3902175"
/tissue type="epithelioid carcinoma"
/tissue type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Not1;
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Average insert size 1.1 kb. Library constructed by Life
Technologies."

/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 707)

Homo sapiens (human)

E I (Dases I CC / CV)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: d column: 16

High quality sequence stop: 688.

Location/Qualifiers

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75.3%; Score 418; DB 10; Length 707; 85.3%; Pred. No. 4.9e-50; ative 0; Mismatches 80; Indels 0
                   Query Match
Best Local Similarity 85.3
Matches 466; Conservative
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BE908201 707 bp mRNA linear EST 20-OCT-2000 601500459F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902175 5',

GI:10402537

mRNA sequence. BE908201 BE908201.1 GI:

ACCESSION VERSION KEYWORDS

BE908201 LOCUS DEFINITION

RESULT

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us-09-938-391-3.rst

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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Eukaryota Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 881)

SNIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

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AGENCOURT 14021788 NIH MGC 179 Homo sapiens cDNA clone
IMAGE:30365831 5', mRNA sequence.
361 CACGGCTCCGACCCCAGCGGGGGCGCCTGACCGACAGCTACTGCGAGACGTGGCGGACG 420
                                                                                                                                    456 GAGGCTCCCTCGGCCACGCCCAGGCCTCCTCCTGCGGGGGCAGGCTCCTGGGGCAG
                                                                                                                                                                                                                                                                                                                                                          516 AGTGCCGCGGGCCTCACCTCACGTCTCTCGCTTCTGGATCAGGAACAGCTTCATGACT 575
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Matches 466; Conservative
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
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/mol type="mRNA"
/db xref="taxon.9606"
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/clone="lorgan: pancreas; Vector: pCMV-SPORT6; Site 1: Not1; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1:1 kb. Library constructed by Life Technologies."
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757 bp mRNA linear EST 20-OCT-2000
601502237F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3904208 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 757)

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov i column: 09
Plate: LLAM9709 row: i column: 09
High quality sequence stop: 757.
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TITLE Direct Submission JOURNAL Submitted (08-DEC-2003) National Inst Gene Collection (MGC), Cancer Genomic Institute, 31 Center Drive, Room 11A, USA NIH-MGC Project URL, http://mgc.ncir Contact: MGC help desk Emall: Gagbs-r@mail.nih.gov Tissue Procurement: Dr. James R. Lups CDNA Library Preparation: Life Techn CDNA Library Arrayed by: The I.M.A.G DNA Sequencing by: Genome Sequence Co BC Cancer Agency, Vancouver, BC, Cana info@bogsc.bc.ca Steven Jones, Jennifer Asano, Ian Bos Steven Jones, Jennifer Asano, Ian Bos Steven Jones, Jentifer Asano, Ian Bos Steven Jones, Jentifer Asano, Ian Bos Steven Jones, Martin Krzywinski, R Sen Lee, Vitcor Ling, Carris Fje Letticia Hsiao, Martin Krzywinski, R Sen Lee, Vitcor Ling, Carris Mathews Netses, Fawan Pandoh, Anna-Linsa Prabh, Michael Thornem, Mirahada Smith, Michael Thornem, Mirahada Smith, George Vand. Scott Zuvderduvr.	BS	Match	3795 TTCTCCTTTGACGCCAAGGACGTCCTGAGGCACCGA 361 CACGGCTCCGACCGGCGCGCCGCCTGACCGA 16
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Bosdet, Yaron Butterfield,
Fjell, Erin Garland, Ran Guin,
Freta Kutsche, Oliver Lee, Soo
ewson, Candice McLeavy, Steven
abhu, Parvaneh Saeedi, Jacqueline
tih, Lorraine Spence, Jeff Stott,
tasja van den Bosch, Jill Vardy,
rco Marra.
                                                                                                                                                                                                                                                                                                                                         ibution information can be found LNL at: http://image.llnl.gov
mn: 6
mpth sequencing because it
said: matched mRNA gi: 18765747
m: frame shifted.
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                                                                .nih.gov
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/organism="Homo sapiens"

/mol_type="mRNN"

/db_xref="taxon:9666"

/dlone="type="teratocarcinoma, cell line"

/tissue_type="teratocarcinoma, cell line"

/tissue_type="teratocarcinoma, cell line"

/tissue_type="teratocarcinoma, cell line"

/lab_host="NHH MGC l109"

/clone lib="NHH MGC l109"

/clone lib="organ: ovary; Vector: poTB7; Site_1: EcoRI; Site_2:

Xhol; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xhol sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Ki (Stratagne) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Butaryota, Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Butaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Butheria; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 944)
S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contect: Robert Strausberg, Ph.D.
Contect: Robert Strausberg, Ph.D.
Email: Capabs-remail.nih.gov
Tissue Procurement: ATCC
CDN Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MgC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LLCM2895 row: d column: 04
High quality sequence stops: 572.
High quality sequence stops: 572.
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
PEAX: 402 762 4306
Email: smith@email.marc.usda.gov
Email: smith@email.marc.usda.gov
strigle pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
plate: TMW8006 row: B column: 3
Seq primer: GTAATACGACTCACTARAGGG.
Location/Qualifiers
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1 (Dases I to S04)

Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Nonneman, D.J., Wray, J.B. and Keele, J.W.

Porcine BST collection using a normalized library constructed from embryos representing early developmental stages
Unpublished (2003)
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Best Local Similarity 89.5%; Pred. No. 4.9e-49;
Matches 442; Conservative 0; Mismatches 52; Indels 0;
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867322 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
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Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wary, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
Contact: Smith T.E.
USDA, ARS, US Meat Animal Research Center
P.D. Box 166, Clay Center, NE 68933-0166, USA
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1 CACACCCACCAGGACTICCAGCTGGT-GCTGCACCTGGTGGCCCTGAACAGCCCGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB444165 650V Bos taurus CDNA 3', mRNA sequence.
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/mol_type="mRNA"
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Tumor Gene Index
Unpublished (1997)

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs.r@mail.nih.gov

Tissue Procurement: James Martin

CDNA Library preparation Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed dy: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, Dento-soares@ulowa.edu

The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                          139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               537 CCACCCTGCCCGTCGTCAACCTCAGGGACGAGGTGCTGTTTCCTAGCTGGGAGGCCTTGT 478
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1 (bases 1 to 703)

NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.

NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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UI-H-FGO-bcp-p-10-0-UI.81 NCI CGAP_ENI_2 Homo sapiens cDNA clone
UI-H-FGO-bcp-p-10-0-UI 3', mRNA sequence.
                                                                      /clone lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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                                                                                                                                                                                                                                                                                                                                                          500 ACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACCTCCTTCTCCAAGTAG 555
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/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
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sequence: 1-44, >POLY A#Simple_repeat (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.

Mol_type="many"

(db_xref="taxon:9606"

(clone="ull-H-FGO-bcp-10-0-UI"

(issue type="many"

(dev_stage="Adult"

(dev_stage="Adult"

(done-lib="OHIOB (life Technologies)"

(clone lib="NOI GAAP ENI_2"

(done lib="NOI GAAP ENI_2"

(done lib="NOI GAAP ENI_2"

(note="Organ: Bone; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR !; Site_2: Not !;

NOI CGAP ENI_2 a cDNA library containing the following tissue(e]: Enchondroma cell line (2 cell lines). The library was constructed according to Bonaido, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site, Double stranded cDNA was ligated to an EcoR adaptor, digested with Not I and cloned directionally into pT773-Pac vector. The oligonaclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)s tail. The sequence tag for this library is CCGGTCACTC. The cell lines was provided by Dr Jame Martin from University of Iowa.

TAG_INB=UI-H-FGO
TAG_ENG_CAGTCACTC. 1. .703
/organism="Homo sapiens" Location/Qualifiers FEATURES

ORIGIN

ö 0; Gaps Query Match 69.3%; Score 384.4; DB 13; Length 703; Best Local Similarity 84.8%; Pred. No. 2.9e-45; Matches 430; Conservative 0; Mismatches 77; Indels 0;

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219 CTGCAGGACCTCTACAGCATCGTGCGCCGCGCCGACCGCACCGGGGTGCCCGTCGTCAAC 160

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TGGCCCCAGAAGAGCGTGTGTGTGTGGCTCGGAACGCGCAAGAGCTGACCGAGAGC 340 TGGCCCCGGAAGAGCGTGTGGCACGCTCCGACCCCAGCGGGCGCCCCTGACCGACAGC TACTGCGAGACGTGGCGGACGGCCCCGGGCGCCACCGGGCAGGCGTCGTCGCTGCTG 459 340 399

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/organism="Homo sapiens"
/organism="Homo sapiens"
/do xref="taxon:9606"
/dlox="IMAGE:6275261"
/clone="IMAGE:6275261"
/lab hof="PHIDB (phage-resistant)"
/lab hof="PHIDB (phage-resistant)"
/lone lib="NIH MGC_102"
/lone lib="NIH MGC_102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: Xho1;
/note="Organ: salivary gland; Vector: poTB7; Site_1: Xho1;
/note="Organ: salivary gland; Vector: poTB7; Site_1: Xho1;
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/note="Organ: salivary gland; Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: Site_1: 929 bp. mRNA linear EST 15-JUL-2002 AGENCOURT 8154946 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275261 BQ672290 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC) BQ672290.1 GI:21783124 Homo sapiens (human) Homo sapiens RESULT 10 BQ672290 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES

9 CACACCCACCAGGACTTCCAGCTGGTGCTGCAGCTGGTGGCCCTGAACAGCCCGCAGCCG 3; Query Match
Best Local Similarity 82.5%; Pred. No. 3.2e-45;
Matches 453; Conservative 0; Mismatches 93; Indels 3;

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ch 67.9%; Score 377; DB 12; Il Similarity 85.5%; Pred. No. 3.2e-44; 419; Conservative 0; Mismatches 71
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UI-E-EO1-ajd-g-02-0-UI.sl UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-ajd-g-02-0-UI3', mRNA sequence.
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The following repetitive elements were found in this cDNA sequence: 1-44, >POLY A#Simple_repeat (matched compliment) Seq primer: M13 Forward POLYA=Yes.
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adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand coNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_INSURE-human fetal eye
TAG_INSURE-human fetal eye
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xd20f03.xl NCI CGAP Ov23 Homo sapiens cDNA clone IMAGE:2594333 3'
similar to SW:CAIH HUMAN P39060 COLLAGEN ALPHA 1(XVIII) CHAIN
SCOXTAINS: ENDOSTATIN];, mRNA sequence.
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1 (bases 1 to 68)

NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/mol_type="mRNN"
/db xref="taxon:9606"
/clone="mRNA"
/db host="MAGE:259433"
/lab host="DH10B"
/lab host="DH10B"
/clone lib="NCI_CGAP_OV23"
/note="Organ: ovary: Vector: pCNV-SPORT6; Site_1: Sall;
/note="Organ: ovary: Vector: pCNV-SPORT6; Site_1: Sall;
/note="Organ: ovary: Vector: pCNV-SPORT6; Site_1: Sall;
/site_2: Not1; Cloned unidirectionally. Primer: Oligo dr.
/Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous; clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCT-CGAP clone distribution information can be
found through the 1.M.A.G.B. Consortium/LibNL at:
www-bio.llnl.gov/bbrp/image/Image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Possible reversed clone: polyT not found
Seg primer: -40UP from Gibco
High quality sequence stop: 408.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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Best Local S
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RESULT 13 BF385854

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BF385854 1007_CGAP_Li9 Mus musculus cDNA clone IMAGE:4195660 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I tbases 1 to 843)
11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/clone="INAGE:4195660"
/lab_host="MAGE:4195660"
/clone lib="NCI CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1:9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Email: cgaper. Strawall.nih.gov.

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High dradial the I.M.A.G.E. Consortium/LLNL at:

High quality sequence start: 23

High quality sequence start: 23

High quality sequence stop: 808.
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                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukarycota; Metazoa; Chordata; Craniata; Vartebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 874)
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                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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Mus musculus (house mouse)
Mus musculus
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                                                                                                         541 TCCTTCTCCAAGIAG 555
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BI412588
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Musualia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1to 4192).

E trausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klauener, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Halah, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.B., Brownstein, M.J., Ugdin, T.B., Toshiyuki, S., Carninci, P., Farnage, C.C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McBwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W., Villalon, D.K., Mazny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Pahey, J., Halton, E., Ketteman, M., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Smailus, D.E., Schnetch, A., Schein, J.E., Schnetch, S., Schnutz, J., Mallah, S., Schnutz, J., Schnutz, M., Schnin, J.E., Schnetch, M., Schein, J.E., Sancher, B.D., Schnetch, S., Schein, J.E., Sancher, M. Schein, J.E., Schnetch, M. Schein, J.E., Schnutz, M. Sancher, M. Schein, J.E., Schnutz, M. Schein, J.E., Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz, M. Schnutz,
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                                                                                                                                                                                                                                                    181 GTGCGCCGCCCGACCGCACCGGGGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 GAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACC 540
                                                                                                                   263 GGGCTGTCGGGCACCTTCCGGGCTTTCCTGTCCTCTAGGCTGCAGGATCTCTATAGCATC 322
                                                                                                                                                                                                                                                                                                                                                  383 CCCAGCTGGGACTCCCTGTTTTCTGGCTCCAGGGTCAACTGCAACCCGGGGCCCGCATC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 TTTTCTTTTGACGGCAGAGATGTCCTGAGACACCCAGCCTGGCCGCAGAAGAGGCGTATGG 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 CACGGCTCCGACCCCAGCGGCCCCCCGACCGACAGCTACTGCGAGACGTGGCGGACG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGCCCAGCTGAAGCCCGGGCCCGCATC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICTCTTTCGACGCAGAGATGTCCTGCAGCACCCCGCTGGCCCCGGAAGAGAGCGTGTGG 360
121 GGGCTGGCCGCCCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 GAGGCCCCGGCCGCCCACCGGCCACGCGTCGTCGCTGCTGGCGGCAGGCTGCTGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              563 daactactegegectacagetcagectectectecteteteagecacedectectegacag
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Mus musculus cDNA clone IMAGE:30354418, containing frame-shift
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Proc. Nail. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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us-09-938-391-3.rst

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NIH-MGC Project URL: http://mgc.nci.nih.gov
Conteat: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Caeavant.
Meb site: http://genome.uiowa.edu
Conteat: bento-soaresewinowa.edu; tom-caeavant@uiowa.edu
Conteat: bento-soaresewinowa.edu; tom-caeavant@uiowa.edu
Bonaddo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A.,
Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K.,
Scheetz, T., Smith, C., Snir, B., Tack, D., Trout, K., Walters, J.,
Caeavant, T., Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: Plate: Row: Column: 0
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13937350
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3562 GGGCTGTCGGGCCCTTCCGGGCTTTCCTGTCTCTAGGCTGCAGGATCTCTATAGCATC 3621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATC 180
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Submitted (26-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/lab_host="bilio"
/note="vector: pYX-ASC"
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3922 AAAGCTGCGAGCTGCCACAACAGCTACATCGTCCTGTGCATTGAGAATAGCTTCATGACC 3981
481 GAGGCGCGAGCTGCCGCCATCGTGGTGCTCTGCATCGAGAACAGCGTCATGACC 540
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Job time : 1706.7 secs
                                                                                                3982 ICTTCTCCAAATAG 3996
                                                                             541 TCCTTCTCCAAGTAG
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein March 26, 2004, 13:28:41; Search time 45.7778 Seconds (without alignments) 1135.676 Million cell updates/sec Run on:

US-09-938-391-4 966 1 HTHQDFQLVLHLVALNSFQP.......CRHAFVVLCIENSVMTSFSK 184 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2001s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

u.	Canine en	Canine pr	Canine an	Murine en	Human End	Human end	Human end				SEQ ID 76	Human end	Human ang			Amino aci	Human end					Human end	Human end	Human HMW	Amino aci
Description		_	_	_						-		Aay08693		Aay90771	Aab16451	Aab30493	Aab49379			m		Aau97132		4	Aab30495
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DB	l w			w	4	m	m	m	4		N	N	m	m	m	m	4	4	S	'n	S	Ŋ	y	m	m
	184	230	184	184	181	182	182	182	182	182	183	183	183	183	183	183	183	183	183	183	183	183	183	195	216
% Query Match Length	100.0	100.0	99.3	88.0	86.4	86.4	Φ	86.4	86.4	86.4	86.4	w	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4		86.4	86.4
Score	996	996	959	850	835	835	835	835	835	835	835	835	835	835	83.5	835	83.5	ิก	ຸຕາ	ന	ന	(1)	835	835	ന
Result No.		63	m	4	ம	9	7	80	თ	10	11	12	13	1.4	12	16	17		16				23	24	52

Aau76689 Synthetic Aau76688 Human col Abg7386 Human Bnd Aby41878 Human alp Aay25113 Human alp Aay25113 Human alp Aay25113 Human alp Aay02515 Human col Aaw92296 Human col Abb83471 Human col Abb83471 Human col Abb83471 Human End Abb83471 Human End Abb83471 Human End Abb83471 Human End Abb83471 Human End Abb83471 Human End Abb83471 Human End Abb83471 Human End Abb8381 Human End Abb8388 Muzine en	7950 9902 8689
AAU76689 AAU76688 AAU76688 AAAU3686 AAAX25113 AAAX25135 AAAX02296 AAAX083308 AAB933471 AAM90877 AAM90879 AAM90877 AAM990877 AAAB49810	AAU7795 ABB7990 AAY0868
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272 3100 6883 6882 1330 1330 1516 1103 1103 1103 1103 1103 1103 1103 11	191 207 184
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	831 831 858
2222888888888884444 9728688888888888888888888888888888888888	4 4 4 4 6 4 6 7 6 4 6

ALIGNMENTS

RESULT 1

Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma, retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; Osler-Webber Syndrome; myocardial angiogenesis; angiofibrona; wound granulation; coronary collateral; oints; erebral collateral; artriovenous malformation; ischaemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiathritic; antipsoriatic; antidiabetic; ophthalmological; AA017430 standard; protein; 184 AA. 19-JUL-2002 (first entry) Canine endostatin. gynaecological AAO17430;

Canis familiaris. EP1191036-A2.

27-MAR-2002.

24-AUG-2001; 2001EP-00307224.

25-AUG-2000; 2000US-0227924P. (PFIZ) PFIZER PROD INC

Tong X; Sheppard MG,

WPI; 2002-354068/39. N-PSDB; AAL46063. An isolated nucleic acid molecule for the treatment of angiogenesis-related disorder, such as cancers or diabetic retinopathy, encodes a endostatin protein.

Claim 14; Fig 5; 56pp; English.

The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration,

corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesie, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine pro-endostatin protein sequence. 8833333338

Sequence 184 AA;

ò 61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVW 120 121 HGSDPSGRRITDSYCETWRTEAPAATGQASSLIAGRLIEQEAASCRHAFVVICIENSVMT 180 121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVWT 180 1 HTHQDFQLVLHLVALNSPQPGGNRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 60 1 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFOQARAAGLAGTFRAFLSSRLQDLYSI 60 Gaps ö 100.0%; Score 966; DB 5; Length 184; 100.0%; Pred. No. 5.6e-107; cive 0; Mismatches 0; Indels 0 Best Local Similarity 100.0 Matches 184; Conservative SFSK 184 Query Match 181 d à g ð q à à

SFSK 184

AAO17429 standard; protein; 230 AA.

AAO17429;

(first entry)

19-JUL-2002

Canine pro-endostatin.

Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; angiofibroma; wound granulation; coronary collateral; citateral; arteriovenous malformation; ischaemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatio; antiarthritic; antipsoriatio; antidiabetic; ophthalmological; gynaecological X PARTE SERVICE Canis familiaris.

EP1191036-A2.

27-MAR-2002.

24-AUG-2001; 2001EP-00307224.

25-AUG-2000; 2000US-0227924P.

(PFIZ) PFIZER PROD INC.

Tong X; Sheppard MG,

2002-354068/39.

N-PSDB; AAL46062

An isolated nucleic acid molecule for the treatment of angiogenesis-related disorder, such as cancers or diabetic retinopathy, encodes an endostatin protein.

Claim 14; Fig 3; 56pp; English.

The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, obler-Webber Syndrome, mycoardial angiogenesis, plaque neovascularisation, telangiectesia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, artificonence and formations, ischaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine pro-endostatin protein sequence

Sequence 230 AA;

ö 47 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 106 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120 107 VRRADRIGVPVVNIRDEVIJPSWEALFSGSEGOLKPGARIFSFDGRDVIQHPAWPRKSVW 166 121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180 9 1 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFOOARRAAGLAGTFRAFLSSRLODLYSI 0; Gaps Query Match 100.0%; Score 966; DB 5; Length 230; Best Local Similarity 100.0%; Pred. No. 7.8e-107; Matches 184; Conservative 0; Mismatches 0; Indels (Query Match à 셤 ઠે 硆 ò

181 SFSK 184

167

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HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT

SFSK 230

RESULT

AAY70265 standard, protein, 184 AA.

AAY70265;

(first entry) 06-JUN-2000 Canine anglogenesis inhibitor, endostatin.

Canine; immunoglobulin Fc fragment; endostatin; immunofusin; anglogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic; antiporiatic; antidiabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; treatment; antiarteriosclerosis; tumour; metastasis; atherosclerosis; psoriasis; rheumatoid arthritis; ocular anglogenic disease; diabetic retinopathy; macular degeneration; wound granulation; keloid scar; gene therapy.

Canis familiaris.

WO200011033-AZ.

02-MAR-2000.

99WO-US019329 25-AUG-1999;

98US-0097883P 25-AUG-1998;

(LEXI-) LEXINGEN PHARM CORP

Lo K, Li Y, Gillies SD;

WPI; 2000-237616/20. N-PSDB; AAZ51309.

New peptide useful for the preparation of medicaments with antiangiogenic activity that may be used in treating tumors or metastases, comprises a sequence corresponding to fragments of human endostatin.

Chillemi F, Vicentinie LMT, Francescato P;

WPI; 2002-698655/75.

sequences corresponding to the human endostatin polypeptide sequence, its salt or non-toxic derivative. The peptides are useful in the preparation of medicaments with antiangiogenic activity which may be useful in treating tumours or metastases. This sequence represents a murine

endostatín polypeptide

Sequence 184 AA;

The invention relates to peptide comprising 20-50 amino acids with

Disclosure; Fig 1; 24pp; English.

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The patent discloses a DNA molecule encoding a fusion protein comprising a signal sequence, an immunoglobulin Fc region, and an angiogenesis can signal sequence an immunoglobulin Fc region, and an angiogenesis continuity or combinations of them. The fusion protein (immunofusin) is activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treated include solid tumours, blood born tumours, tumour metaetasis, benign tumours including mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metaetasis, benign tumours including care undour activity for the protein of seases of diabetic retinopathy, retinopathy of prematurity, macular angiogenic diseases diabetic retinopathy, retinopathy of prematurity, macular elements of diseases can observate and osler-Webber syndrome; myocardial angiogenesis, plangue neovascular fastion, telangietisals, hemophiliac joints, and excessive or abnormal stimulation of endothelial cells, intestinal cells, atherosclerosis, sclerodermal and hypertrophic scarse, i.e. Rebloid scars: The DNA constructus may be used in gene therapy. The present sequence is a canine endostatin used in the construction of immunofusin containing canine immunoglobulin Fc fragment
Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration.
                                                                                                                    Example 8; Page 59-60; 68pp; English
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9 9

61 VRRADRAAVPIVNLKDELLFPSWEALFSGSEGPLKPGARIFSFDGKDVLRHPTWPQKSVW 120 VRRADRIGVPVVNLRDBVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVW 120

61

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1 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFOQARAAGLAGTFRAFLSSRLQDLYSI

88.0%; Score 850; DB 5; Length 184; 85.3%; Pred. No. 4.4e-93; Live 14; Mismatches 13; Indels

Matches 157; Conservative

Local Similarity

Query Match

121 HGSDPSGRRITDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180

181 SFSK 184

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                                                                                                                                            61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120
                                                                                                                                                                             61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVW 120
                                                                                                                                                                                                                  HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180
                                                                                                                                                                                                                                       1 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 60
                                                                                               1 HTHQDFQPVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI
                                        Gaps
                                     .
0
99.3%; Score 959; DB 3; Length 184; 99.5%; Pred. No. 3.9e-106; Live 0; Mismatches 1; Indels
                                   183; Conservative
                   Similarity
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endostatin; tumour; cancer; metastasis; cytostatic;
          ABG31794 standard; protein; 184 AA.
                                               Murine endostatin polypeptide
                                    05-DEC-2002 (first entry)
                                                                  antianglogenic
                       ABG31794;
                                                            Mouse;
RESULT 4
      ABG31794
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27-FEB-2002; 2002WO-IT000119 27-FEB-2001; 2001IT-MI000394

WO200268457-A2.

Mus sp

06-SEP-2002

(UYMI-) UNIV MILANO.

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Human; Endostatin(TW); anglogenesis mediated disease; solid tumours; blood borne tumour; leukaemia; tumour metastasis; benign tumour; baemangioma; acoustic neuroma; neurofibroma; trachoma; rubeosis; progranto granuloma; rheumatoid archritis; psoriasis; coular anglogenic disease; diabetic retinopathy; macular degeneration; retinopathy of prematurity; macular corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; cterminus minus 2 protein.
                                                                                                                                                                       Human Endostatin(TM) C-terminus minus 2 protein.
                                                                          AAU00898 standard; protein; 181 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0153698P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-SEP-2000; 2000WO-US025166
                                                                                                                                        04-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ENTR-) ENTREMED INC.
181 AFSK 184
                                                                                                                                                                                                                                                                                                                                                                                                          WO200119989-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-2001
                                                                                                          AAU00898;
                                             RESULT
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Boerner RJ;

Zhou X, Madsen J,

Chang-Murad A, Zh FR, Shepard SR,

Sim KL,

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The sequence represents Human Endostatin(TM) C-terminus minus 2 protein,
a natural variant lacking the C-terminal 2 amino acids of Endostatin(TM)
c recovered from fermentations of Pichia patorists cultures harbouring a
expression plasmid containing the Endostatin(TM) DNA sequence given in
AAS00867. The new method of the invention is useful for producing,
c recovering and purifying Endostatin (TM) from biological sources, such as
biological fluids, tissues, cells, culture media, and fermentation media.
Endostatin(TM) is useful for treating angiogenesis mediated diseases,
biological fluids, tissues, cells, culture media, and fermentation media.
Endostatin(TM) is useful for treating angiogenesis mediated diseases,
benign tumours, e.g. haemangioma, rounell arthitis, psoriasis,
c trachomas, and pyogenic granulomas, rheumatoid arthitis, psoriasis,
c trachomas, and pyogenic granulomas, rheumatoid arthitis, psoriasis,
c trachomas, colon cancer, retrolental fibroplasia, rubecsis, Osler-Webber
CS yndrome, myocardial angiogenesis, plaque neovascularisation,
c plangiectasia, haemophiliac joints, angiofibroma, and wound granulation.
c telangiectasia, haemophiliac joints, angiofibroma, and wound granulation.
c telangiectasia, haemophiliac joints, angiofibroma, and wound granulation.
c telangiectasia, neovocardam and hypertrophic scars. Higher yields of
more purified, and biologically active Endostatin(TM) are obtained by the
c new method. Endostatin(TM) can be stored in buffers for extended periods
of time, and also subjected to lyophilisation, while preserving
c production is avoided, preventing unwanted potential cellular lysis and
contamination with additional proteins, pigments, enzymes and other
                                                                                                                                                                                Producing Endostatin protein for treating angiogenesis mediated diseases such as solid tumors, comprises recombinantly producing the protein using an expression system, and recovering and purifying the protein.
                                                                                                                                                                                                                                                                                               Claim 5; Page 30; 67pp; English
                                                      Bermejo LL, Mistry FR,
                                                                                                      WPI; 2001-244802/25
                                                                                                                                   N-PSDB; AAS00867
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Sequence 181 AA;

ö 120 120 180 180 9 9 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 1 HTHODFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW Gaps . 0 86.4%; Score 835; DB 4; Length 181; 85.1%; Pred. No. 2.7e-91; ive 14; Mismatches 13; Indels Best Local Similarity 85.18 Matches 154; Conservative S 181 A 181 181 d à 셤 엄 ò $\stackrel{>}{\circ}$

AAY59622 standard; protein; 182 AA AAY59622; RESULT 6
AAY59622
ID AAY5
XX
AC AAY5
XX
DT 14-h
XX
XX
XX
XX
XX
XX
XX

Human endostatin protein fragment (first entry) 14-MAR-2000

This sequence is a fragment of the human endostatin protein. Endostatin is an approximately 20kD C-terminal globular domain of the collagen-like protein collagem XVIII. Protein oligomers consisting of more than one endostatin collagem XVIII. Protein oligomers consisting of more than one endostatin monomer have anti-tubulogenic effects and induce controlly and inhibit tubulogenic effects. The oligomers can also be used to treat metastatic cancers, tumours, closuration of cells, and inhibit tubulogenesis and tumourigenesis. The oligomers can also be used to treat metastatic cancers, tumours, columnatoid arthritis, psoriasis, coular angiogenic disease, obsler-Webber syndrome, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma and wound granulation. The oligomers can also be used to creat diseases that have angiogenesis as a pathological consequence e.g. ulcers. The endostatin oligomers can also be used to columns for isolating antibodies or receptors. Passive antibody therapy columns for isolating antibodies or receptors. Passive antibody therapy columns antibodies that specifically bind endostatin digomer as well as angiogenesis-dependent processes such as reproduction, development, wound antisera directed to the Pab regions of endostatin oligomer antibodies can be administered to the Pab regions of endostatin oligomer antibodies can be administered to bind endostatin oligomers. Endostatin, scatter factor activity, human, tubulogenesis, psoriasis, metastatic cancer, tumourigenesis, ocular angiogenic disease, rheumatoid arthritis, Osler-Webber syndrome, telangiectasia; haemophiliac joint; angiofibroma; wound granulation. New endostatin oligomers, used for treating e.g. tumors Disclosure; Page 6; 44pp; English. (CHIL-) CHILDRENS MEDICAL CENT 98US-0087890P. 98US-0092393P. 98US-0098790P. 99WO-US012278 Javaherian K, Folkman MJ; WPI; 2000-072833/06. Sequence 182 AA; WO9962944-A2. Homo sapiens 03-JUN-1999; 03-JUN-1998; 10-JUL-1998; 09-DEC-1999

ö 9 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGIAGTFRAFLSSRLQDLYSI ; ; Score 835; DB 3; Length 182; ; Pred. No. 2.7e-91; 14; Mismatches 13; Indels 86.4%; 85.1%; Cuery Match Best Local Similarity 85.1% Marches 154; Conservative ò

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181 S 181

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RESULT

us-09-938-391-4.rag

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HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Page 291-292; 298pp; English
                                                                                                                                                    AAB28399 standard; protein; 182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-2000; 2000WO-US011367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 154; Conservative
                                                                                                                                                                                                        19-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thorpe PE, Brekken RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-687317/67.
                                                                                                                                                                                                                                     Human endostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 182 AA;
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A 181
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                                                        181 S 181
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                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                    181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is an endostatin protein which is the carboxy terminal protein of human collagen XVII. Recombinant mouse endostatin (10 mg/kg) was administered subcutaneously to mice implanted with Lewis lung carcinomas. There was tumour mass regression non-detectable levels after 12 days of therapy due to the anglogenesis inhibitory activity of endostatin. Thus the protein is useful for treatment of anglogenesis. Compared to the cancer the polynucleotide and polypeptide sequences of this endostatin are useful for treating and diagnosis of tumours, ocular cangingenic diseases. Osler-webber syndrome, myccardial anglogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, anglofibroma and wound granulation of endothellal cells e.g. intestinal excessive or abnormal stimulation of endothellal cells e.g. intestinal as a birth control agent by reducing or preventing uterine as a birth control agent by reducing or preventing uterine cells, by classue that express high levels of endostatin, eg. tumour cells, by generating cDNA from mRNA using reverse transcriptase and then amplifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel endostatin capable of inhibiting endothelial cell proliferation and angiogenesis, useful for treating angiogenesis-dependent cancers and as birth control agents.
                                                                                                                          Human, endothelial cell proliferation inhibitor; collagen XVIII; anglogenesis inhibitor; anti-tumour; cytostatic; antipsoriatic; vasotropic; determatological; ophthalmological; vulnerary; antidiabetic; hamostatic; contraceptive; contraceptive; collar angiogenic disease; atherosclerosis; soleroderma; myocardial angiogenesis; telangiectasia; angiofibroma; wound granulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 + SHRDFQPVLHLVALNSPLSSGARGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HTHODFOLVIHIVALNSPOPGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLODLYSI
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                  AAY94323 standard; protein; 182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 38; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                           (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                    98US-0106343P.
99US-00315689.
                                                                                                                                                                                                                                                                                                           99WO-US025605
                                                                       11-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.14
Best Local Similarity 65.14
Matches 154; Conservative
                                                                                                    Human endostatin protein.
                                                                                                                                                                                                                                                                                                                                                                                                         O'reilly MS, Folkman MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-365617/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA27004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 182 AA;
                                                                                                                                                                                                                                                     WO200026368-A2
                                                                                                                                                                                                                                                                                                                                     30-OCT-1998;
20-MAY-1999;
                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                           01-NOV-1999;
                                              AAY94323;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VRRADRIGVPVVVILRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HTHODEOLVLALVALNSPORGARGIRGADEOCFOGARAAGLAGTERAFLSSKLODLYSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; endostatin; cytostatic; antiproliferative;
vascular endothelial growth factor; VEGF; antibody; VEGF2 receptor;
cancer; vascularised solid tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic composition for the treatment and diagnosis of cancer comprises an anti-VEGF (vascular endothelial growth factor) antibo binding the same epitope as the monoclonal antibody ATCC PTA 1595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 86.4%; Score 835; DB 3; Length 182; Local Similarity 85.1%; Pred. No. 2.7e-91; Local Similarity 85.1%; Pred. No. 2.7e-91; Indels tes 154; Conservative 14; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S 181
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us-09-938-391-4.rag

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Gaps

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Human Endostatin(TM) C-terminus minus 1 protein.
       AAU00897 standard; protein; 182 AA.
                                                                                                                                                                         Claim 5; Page 30; 67pp; English.
                                                                                                          14-SEP-2000; 2000WO-US025166.
                      (first entry)
                                                                                                                                     Mistry FR,
                                                                                                                         ENTR-) ENTREMED INC.
                                                                                                                                            WPI; 2001-244802/25.
                                                                                                                                 Sim KL,
                                                                                                                                                 N-PSDB; AAS00897
                                                                                         WO200119989-A2
                                                                                                                 14-SEP-1999;
                                                                                  Homo sapiens
                      04-JUL-2001
                                                                                                  22-MAR-2001
                                                                                                                                     Bermejo LL,
               AAU00897;
                                                                                                                                 Liang H,
RESULT 9
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99US-0153698P

Human, immunoconjugate, anti-vascular endothelial growth factor antibody; anti-VEGF antibody, 2C3 ATCC PTA 1555, VEGF receptor; VEGFR2, KOK/FIK-1, VEGFR1, FIL-1, angiogenesis, macular degeneration; ocular neovascular disease, cancer; vascularised solid tumour; AIDS; metastatic tumour; endothelial cell proliferation; inflammatory disorder; atheroselerosis; diabetic retinopathy; corneal graft rejection; acquired immune deficiency syndrome; infection; restenosis; fungal ulcer; sickle cell anaemia; endometriosis; endostatin. The present invention relates to antibody-based compositions comprising an immunoconjugate such as anti-vascular endothelial growth factor (WBGF) antibody (Ab) (or its antigen-binding fragment), attached to a biological agent, where the Ab binds to the same epitope as the monoclonal antibody (MAD) 2C3 ATCC PTA 1595, and significantly inhibits WBGF binding to the Immunoconjugate compositions for treating cancer by inhibiting angiogenesis and for delivering a diagnostic agent to tumor, comprises anti-vascular endothelial growth factor antibody attached to a biological 61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI contamination with additional proteins, pigments, enzymes and other cellular chemicals and debris ö Length 182; Example 10; Page 12-13 (Sequence listing); 299pp; English. 13, Indels 86.4%; Score 835; DB 4; 85.1%; Pred. No. 2.7e-91; iive 14; Mismatches 13 Amino acid sequence for human endostatin. AAU77951 standard; protein; 182 AA. 12-OCT-2001; 2001AU-00079401. 28-APR-2000; 2000AU-00048049. (TEXA) UNIV TEXAS SYSTEM. 02-JUL-2002 (first entry) Query Match Best Local Similarity 85.1³ Matches 154; Conservative Thorpe PE, Brekken RA; WPI; 2002-281368/33. Sequence 182 AA; AU200179401-A. 181 S 181 181 A 181 Homo sapiens. 06-DEC-2001. AAU77951; agent. RESULT 10 88333 g g ð 셤 ઠે à à The sequence represents Human Endostatin(TM) C-terminus minus 1 protein,
a natural variant lacking the C-terminal amino acid of Endostatin(TM)
c recovered from fermentations of Pichia pastoris cultures habbouring a
expression plasmid containing the Endostatin(TM) DNA sequence given in
AASO0867. The new method of the invention is useful for producing,
c recovering and purifying Endostatin (TM) from biological sources, such as
biological fluids, tissues, cells, culture media, and fermentation media.
Endostatin(TM) is useful for treating angiogenesis mediated diseases such
as solid tumours, blood borne tumours, leukaemias, tumour mediated
c solid tumours, e.g. haemangioms, rheumatoid arthritis, psoriasis,
c benign tumours, e.g. haemangioms, rheumatoid arthritis, psoriasis,
c trachomas, and pyogenic granulomas, rheumatoid arthritis, psoriasis,
c trachomas, and pyogenic granulomas, reteminatedry, retinopathy of
prematurity, macular degeneration, corneal graft rejection, neovascular
c plantome, myocardial angiogenesis, plaque neovascularisation,
c clangicctasis, heemophiliac joints, angiofibroma, and wound granulation.
c clangicctasis, heemophiliac joints, angiofibroma, and wound granulation.
c clangicctasis, scleroderme and hypertrophic scars. Higher yields of
atherosclerosis, scleroderme and hypertrophic scars. Higher yields of
more purified, and biologically active Endostatin(TM) are obtained by the
method. Endostatin(TM) can be stored in buffers for extended periods
of time, and also subjected to lyophilisation, while preserving
blological activity. Centrifugation of broth from fermentation steps in
production is avoided, preventing unwanted potential cellular lysis and Producing Endostatin protein for treating angiogenesis mediated diseases such as solid tumors, comprises recombinantly producing the protein using an expression system, and recovering and purifying the protein. Human; Endostatin(TM); angiogenesis mediated disease; solid tumours; blood borne tumour; leukaemia; tumour metastasis; benign tumour; haemangioma; accussic neuroma; neurofithroma; trachoma; rubeosis; pyogenic granuloma; rheumatoid arthritis; psoriasis; colon cancer; ocular angiogenic disease; diabetic retinopathy; macular degeneration; retinopathy of prematurity; macular corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; oblar-webber Syndrome; myocardial angiogenesis; plaque neovascularisation; relangiactasia; haemophiliac joint; angiofibroma; wound granulation; variant; Chang-Murad A, Zhou X, Madsen J, Boerner RJ; y FR, Shepard SR, Schrimsher JL;

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VEGF receptor VEGFR2 (KDR/FIk-1) without inhibiting VEGF binding to the VEGF receptor VEGFR3 (FIL-1). The compositions of the invention are useful in therapy, and diagnosis, for inhibiting angiogenesis in an animal having ocular neovaecular disease or macular degeneration, and for delivering a biological agent to a vascularised tumour. The compositions or avacularised solid tumour, a metastatic tumour or metastases from a primary tumour. The composition is useful for specifically inhibiting VEGF-induced endothelial cell proliferation, without significantly inhibiting VEGF-induced macrophage, osteoclast or chondroclast function. The composition streaming various diseases such as inflammatory disorders, atherosclerosis, disbectic retinopathy, restenosis, acquired immune deficiency syndrome (AIDS), blood borne tumours, corneal graft rejection, Crohn's disease, fungal ulcers, infections human endostatin. Endosmetiosis. The present sequence represents human endostatin. Endosmetin may be attached or functionally associated with anti-VEGF antibodies

Sequence 182 AA;

61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120 61 VRRADRAAVPIVNLKDELLFPSWEALFSGSBGPLKFGARIFSFDGKDVLRHFTWPQKSVW 120 9 1 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 60 1 HSHRDFQPVLHLVALNSPLSGGNRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSI , 0 Query Match 86.4%; Score 835; DB 5; Length 182; Best Local Similarity 85.1%; Pred. No. 2.7e-91; Matches 154; Conservative 14; Mismatches 13; Indels A 181 S 181 181 181 q à 셤 ò 셤

AAY02113 standard, protein; 183 AA. 16-JUL-1999 (first entry) SEQ ID 76 of WO9916889 AAY02113; RESULT 11 AAY02113

Angiostatin; endostatin; interferon; thrombospondin; interferon-inducible protein; platelet factor 4; anti-angiogenic; anti-tunor; multifunctional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis; tumor cell production.

Homo sapiens

08-APR-1999.

98WO-US020464. 30-SEP-1998;

Casperson GF, Bolanowski MA, Caparon MH, Mckearn JP; S CO G D (SEAR) SEARLE

Klein BK;

Gregory SA,

WPI; 1999-255098/21

The specification describes multifunctional proteins which comprise combinations of angiostarin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have antiangiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence is multifunctional proteins useful for treating angiogenic-mediated Disclosure; Page 106-107; 121pp; English.

Sequence 183 AA;

ö 120 61 VRRADRAAVPIVNLKDELLFPSWEALFSGSEGPLKPGARIFSFDGKDVLRHPTWPQKSVW 120 121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180 9 61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVW 1 HTHQDFQLVLHLVALNSPQPGGWRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI Query Match

Best Local Similarity 85.1%; Pred. No. 2.8e-91;
Matches 154; Conservative 14; Mismatches 13; Indels : A 181 181 S 181 181

ò 엄 ò d ò g AAY08693 standard; protein; 183 AA. (first entry) 10-AUG-1999 AAY08693;

Human endostatin protein fragment.

Plasminogen; human; angiostatin; endostatin; gene therapy; vector; anti-angiogenic; attenuation; cytostatic; anti-diabetic; ophthalmology; tumour growth; solid tumour; diabetic retinopathy; retina. WO9926480-A1. 03-JUN-1999.

(GENE-) GENETIX PHARM INC. (MASI) MASSACHUSETTS INST TECHNOLOGY. 97US-00975424 20-NOV-1997;

98WO-US024950

20-NOV-1998;

Bachelot T; Pawliuk RJ, Leboulch P,

Mon Mar 29 17:32:22 200

This invention describes a novel viral gene therapy vector comprising a nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine angiogentin, human or murine endostatin and angiogenesis-inhibiting fusions and fragments, where the viral vector is sufficiently attenuated for use in human gene therapy. The products of the invention have anti-angiogenic, cytostatic, anti-diabetic and ophthalmological activity. The vector is used in gene therapy for inhibiting tumour growth in humans harbouring a solid tumour. The vector expresses an anti-angiogenic polypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis in the vicinity of the retina. The vector is administered to cells exvivo and then administered to the patient Disclosure; Page 74-75; 83pp; English. Anti-angiogenic gene therapy vectors. WPI; 1999-357696/30, N-PSDB; AAX77719.

Sequence 183 AA;

VRRADRIGVPVVNLRDEVLPPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120 VRRADRAAVPIVNLKDELLFPSWEALFSGSEGPLKFGARIFSFDGKDVLRHFTWPQKSVW 120 121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180 9 1 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 60 1 HSHRDFQPVLHLVALNSPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSI 0; Gaps Ouery Match 86.4%; Score 835; DB 2; Length 183; Best Local Similarity 85.1%; Pred. No. 2.8e-91; Matches 154; Conservative 14; Mismatches 13; Indels 181 S 181 g qq g ò ð ò

Human angiogenesis inhibitor, endostatin. AAY70252 standard; protein; 183 AA. 06-JUN-2000 (first entry) RESULT 13

Human, immunoglobulin gamma Fo fragment, endostatin, immunofusin, angiogenesis, inhibitor; cytostatic, antitheumatoid; antiarthritic; antiporiatic, antidiabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; treatment; antiarteriosclerosis; tumour; metastasis; atherosclerosis; psoriasis; rheumatoid arthritis; ocular angiogenic disease; diabetic retinopathy; macular degeneration; wound granulation; keloid scar; gene therapy.

WO200011033-A2.

02-MAR-2000

98US-0097883P, 25-AUG-1998;

(LEXI-) LEXINGEN PHARM CORP.

Li Y, Gillies SD; WPI; 2000-237616/20. 5 K

N-PSDB; AAZ51291

Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration.

Example 1; Page 41-42; 68pp; English.

a signal sequence, an immunoglobulin For region, and an angiogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The twison protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, henign tumours including has acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, rehematorid arthritis, psoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibrace neovascularisation, telangictesia, hasmophiliac joints, angiofibroma, wound granulation, the amenophiliac joints, angiofibroma, wound granulation, and excessive or abnormal stimulation of endothelial caras, incertinal cells, atherosclerosis, sclerodermal and hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a human endostatin used in the construction of immunofusin containing human immunoglobulin gamma (19G) The patent discloses a DNA molecule encoding a fusion protein comprising

Sequence 183 AA;

ð g ò a ò 셤

ö 61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120 61 VRRADRAAVPIVNIKDELLFPSWEALFSGSEGPLKPGARIFSFDGKDVLRHFTWPQKSVW 120 121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180 9 1 HSHRDFÖPVIHIVAINSPISGGMRGIRGADFÖCFÖGARAVGLAGTFRAFISSRIQDIYSI 60 1 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLODLYSI 0; Gaps 86.4%; Score 835; DB 3; Length 183; 85.1%; Pred. No. 2.8e-91; Live 14; Mismatches 13; Indels Best Local Similarity 85.1% Matches 154; Conservative Query Match

181 S 181 181 A 181 ò

AAY90771 standard; protein; 183 AA. 22-AUG-2000 (first entry) AAY90771;

Human angiogenesis inhibiting factor 1 protein.

Human; angiogenesis inhibiting factor 1; IAF-1; tumour; antibody; abnormal vessel disease.

Homo sapiens

CN1244536-A.

98CN-00117150. 98CN-00117150

Angiogenesis inhibiting factor 1 and its derivative useful for treating (ONCO-) INST ONCOLOGY UNDER TUMOR HOSPITAL CHINE. Claim 1; Fig 5; 41pp; Chinese 2000-388168/34 WPI; 2000-388168, N-PSDB; AAA29884 Guo W; A 181 10-AUG-1998; 10-AUG-1998; AAB16451; 61 121 181 Query Match Best Local Matches 15 fang Z, RESULT 1 ઠે Вb ò ò g

The present sequence represents an angiogenesis inhibiting factor (1), designated IAF-1. The present invention also describes: (1) preparation of (1) and its derivative; (2) an IAF binding acceptor and its preparation; and (3) an IAF antibody. (1) is useful for preparing new biological preparations for effectively treating various tumours and abnormal-vessel diseases. The IAF antibody is preferably a polyclonal antibody, mosaic antibody, single stranded antibody and human originated . 0 86.4%; Score 835; DB 3; Length 183; 85.1%; Pred. No. 2.8e-91; ive 14; Mismatches 13; Indels al Similarity 85.1 154; Conservative Sequence 183 AA;

61 VRRADRAAVPIVNLKDELLFPSWEALFSGSEGPLKPGARIFSFDGKDVLRHPTWPQKSVW HGSDPSGRRLTDSYCETWRTEAPATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 1 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 181 S 181

AAB16451 standard; protein; 183 AA. 27-OCT-2000

(first entry)

Human endostatin protein sequence.

Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin; endostatin; plasminogen; laminin; treatment; wound healing; solid tumour; psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease; cerebral collateral; arteriovenous malformation; rubeosis; cancer; diabetic retinopathy; arthrits; wound healing; peptic ulcer; Helicobacter related disease; fracture; cat scratch fever.

sapiens Кошо

08-JUN-2000

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This invention relates to angiogenesis-inhibiting protein receptors, and the DNA sequences encoding them. Angiogenesis is the generation of new blood vessels into a tissue, and normally occurs in wound healing, foetal and embryonal development and the formation of the corpus luteum, condemetrium and placenta. Angiostatin is a protein (see AAB16450 and AAA88202) involved in angiogenesis, and has an amino acid sequence similar to that of a plasminogen fragment (see murine plasminogen con AAA88203). Angiostatin has the ability to inhibit angiogenesis.

CAAB16490). Angiostatin has the ability to inhibit angiogenesis.

CAAB16303). Sequences AAA88242 and AAB16522 represent coding and protein sequences of human laminin. Laminin is an angiostatin binding protein.

CON AAA88203 is and protein receptor fragments of the invention. The angiogenesis-inhibiting protein receptor fragments of the invention. The confides bind either angiostatin or endostatin and can be used in methods of the tracting protein and can be used in methods contracting in diseases and processes that are mediated by angiogenesis, crohn's diseases and processes that are mediated by angiogenesis, crohn's diseases and processes that are mediated by angiogenesis, crohn's diseases and processes that are mediated by angiogenesis, crohn's diseases and processes that are mediated by angiogenesis, crohn's diseases seek, fractures, placentation and cat scratch fever. They are useful for the detection and prognosis of cancer. DNA sequences A628204-A628241 encode the peptides of the invention
                                                                                                                                                                                                                                                 New angiogenesis-inhibiting protein receptors, useful in methods for treating diseases and processes that are mediated by angiogenesis, s as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 3; 100pp; English
99WO-US028897
                                                    98US-00206059
                                                                                                      (ENTR-) ENTREMED INC
                                                                                                                                                                                                        WPI; 2000-412290/35.
                                                                                                                                                        Macdonald NJ,
06-DEC-1999;
                                                    04-DEC-1998;
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Gaps ÷ 86.4%; Score 835; DB 3; Length 18 85.1%; Pred. No. 2.8e-91; ative 14; Mismatches 13; Indels Conservative Local Similarity Matches 154; Query Match

Sequence 183 AA;

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1 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI

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120 121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180 61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 1 HSHRDFQPVLHLVALNSPLSGGMRGIRGADFQCFQQRAAVGLAGFFRAFLSSRLQDLYSI 셤 qq 원 ò ò

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RESULT 2
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'Sequence 14, Application US/09561108
'Patent No. 6342221
'GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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NS-09-51-500-14

Sequence 14, Application US/09561500

Patent No. 643-21-201

APPLICANT: Philip E. Thorpe

APPLICANT: Philip E. Thorpe

APPLICANT: Philip E. Thorpe

TITLE OF INVENTION: ANTHEODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF

PILE REFERENCE: 4001.002500

CURRENT FILING DATE: 2000-04-28

PRIOR PILING DATE: 1990-04-28

NUMBER OF SEQ ID NOS: 44

SOFFWARE: PatentIN Ver. 2.0

SEQ ID NO 14

LENGTH: 182

***LENGTH: 182

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Sequence 14, Application US/09561526
| Sequence 14, Application US/09561526
| Patent No. 641678
| GENERAL INFORMATION:
| APPLICANT: Philip E. Thorpe
| APPLICANT: Philip E. Thorpe
| TITLE OF INVENTION: ANTIODY CONJUGATE KITS POR SELECTIVELY INHIBITING VEGF
| TITLE OF INVENTION: ANTIODY CONJUGATE KITS POR SELECTIVELY INHIBITING VEGF
| CURRENT APPLICATION NUMBER: US/09/561,526
| CURRENT FILING DATE: 2000-04-28
| FRIOR APPLICATION NUMBER: 60/131,432
| PRIOR APPLICATION NUMBER: 60/131,432
| NUMBER OF SEQ ID NOS: 44
| SOFTWARE: PATENTIN Ver. 2.0
| SEQ ID NO 14
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US-05-561-499-14
US-09-561-499-14

US-09-561-499-14

Sequence 14, Application US/09561499

Patent No. 6524583

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTHEODY METHODS FOR SELECTIVELY INHIBITING VEGF

TITLE REFERENCE: 4001.002582

CURRENT APPLICATION NUMBER: US/09/561,499

CURRENT APPLICATION NUMBER: 60/131,432

PRIOR FILING DATE: 1995-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 14

LENGTH: 182
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121 HGSDPNGRRLTESYCETWRTEAPSATGQASSLLGGRLLGQSAASCHHAYIVLCIENSFMT
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ORGANISM: Artificial Sequence
FEATURE:
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     APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
APPLICANT: Rolf A. Brekken
APPLICANT: Rolf A. Brekken
APPLICANT: Rolf A. Brekken
FILE COF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REPERENCE: 4001.002584
CURRENT APPLICATION NUMBER: US/09/561,108
FROR APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
PRIOR FILING DATE: 1999-04-28
SCOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 182
TYPE: PRI
TYPE: PRI
TYPE: PRI
ORGANISM: Artificial Sequence
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Patent No. 6346510
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FOLKman, Judah
APPLICANT: FOLKman, Judah
TITLE OF INVENTION:
FILE REPERENCE: 6213-0229
CURRENT APPLICATION UNMER: US/09/315,689
CURRENT APPLICATION UNMER: US/09/315,689
CURRENT APPLING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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86.4%; Score 835; DB 4; Length 182;
Best Local Similarity 85.1%; Pred. No. 7e-96;
Matches 154; Conservative 14; Mismatches 13; Indels
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. OTHER INFORMATION: Description of Artificial Sequence:
. OTHER INFORMATION: PEPTIDE
US-09-561-108-14
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CRGANISM: Homo sapiens
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TYPE: PRT ORGANISM: Artificial Sequence
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APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
TITLE OF INVENTION: INHIBITING VEGF
FILE REPERRORS: 4001.002584
CURRENT APPLICATION NUMBER: US/09/998,831
CURRENT APPLICATION NUMBER: US/09/998,831
PRIOR APPLICATION NUMBER: 09/561,108
PRIOR APPLICATION NUMBER: 09/561,108
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE PATENTIN VET. 2.0
SOFTWARE PATENTIN VET. 2.0
                                                                                                                                          1 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFQQARAAGLAGTFRAFLSSRLQDLYSI
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CTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
FOTHER INFORMATION: PEPTIDE
CAS-09-998-831-14
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86.4%; Score 815; DB 4; Length 182;
Best Local Similarity 85.1%; Pred. No. 7e-96;
Matches 154; Conservative 14; Mismatches 13; Indels
                                                          Query Match

86.4%; Score 835; DB 4; Length 182;
Best Local Similarity 85.1%; Pred. No. 7e-96;
Matches 154; Conservative 14; Mismatches 13; Indels
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Patent No. 6676941
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US-09-206-059-2
; Sequence 2, Application US/09206059
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ORGANISM: Artificial Sequence
; OTHER INFORMATION: PEPTIDE US-09-561-499-14
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US-09-998-831-14
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Sequence 13, Application US/09561500

Sequence 13, Application US/09561500

Sequence 13, Application US/09561500

GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe

APPLICANT: Philip E. Thorpe

APPLICANT: Philip E. ANTIBEDY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF

FILE REPERENCE: 4001.002500

CURRENT APPLICATION NUMBER: 00/09/561,500

CURRENT PRILING DATE: 2000-04-28

PRIOR PRILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SOGTWARE: Patentin Ver. 2.0

SEQ ID NO 13

LENGTH: 191
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-561-500-13
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Best Local Similarity 85.1%; Pred. No. 7.18-96;
Matches 154; Conservative 14; Mismatches 13; Indels
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OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
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ORGANISM: Artificial Sequence
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US-09-998-831-13
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Patent No. 634221
Patent No. 634221
APPLICANT: Philip E. Thorpe
APPLICANT: Poil M. Brekken
TITLE OF INVENTION: ANTIBODY CONUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
CURRENT APPLICATION NUMBER: US/09/561,108
CURRENT APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
SPRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
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Squarce 13, Application US/09561526

Squarce 13, Application US/09561526

GENERAL INFORMATION:

APPLICANT: Philip B. Thorpe

APPLICANT: Rolf A Brekken

TITLE OF INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF

TITLE OF INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF

CURRENT APPLICATION NUMBER: US/09/561,526

CURRENT PILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SGOFFWARE: PatentIn Ver. 2.0

SEQ ID NO 13

LENGTH: 191
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121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180
                   61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 86.0%; Score 831; DB 4; Length 191; Best Local Similarity 83.7%; Pred. No. 2.4e-95; Matches 154; Conservative 17; Mismatches 13; Indels
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ORGANISM: Artificial Sequence
PEATURE:
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US-09-561-108-13
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LENGTH: 191
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68 VRRADRGSVPIVNLKDEVLSPSWDSLFSGSQGQLQPQARIFSFDGRDVLRHPAWPQKSVW 127
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Sequence 13, Application US/09561499

Sequence 13, Application US/09561499

Patent No. 6524633

GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: Roif A. Brekken

TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF

TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF

TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF

FILE REPREBRUCE: 4001.003582

CURRENT FILING DATE: 2000-04-28

FRIOR PELING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE PATENTION OF SEQ ID NOS: 44

SOFTWARE PATENTION OF SEQ ID NOS: 44

SEQ ID NO 13

LENGTH: 191
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Query Match 86.0%; Score 831; DB 4; Length 191; Best Local Similarity 83.7%; Pred. No. 2.4e-95; Matches 154; Conservative 17; Mismatches 13; Indels
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APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: INHIBOTY CONJUGATE COMPOSITIONS FOR SELECTIVELY
TITLE OF INVENTION: INHIBITING VEGF
FILE REFERENCE: 4001.002584
CURRENT APPLICATION NUMBER: US/09/998,831
CURRENT FILING DATE: 2001-11-30
PRIOR PILING DATE: 2001-11-30
PRIOR PILING DATE: 200-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: 200-04-28
LENGTHAR: 191
LENGTH: 191
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83.7%; Pred. No. 2.4e-95;
tive 17; Mismatches 13; Indels
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US-08-159-784-2
Sequence 2, Application US/08159784
Patent NO. 5643783
GENERAL INFORMATION:
APPLICANT: BJOOT R. Olsen
TITLE OF INVENTOR: 9
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE FISHS & Richardson
STREET: 225 Franklin Street
CITY: Boston
STREET: Assachusetts
COUNTRY: U.S.A.
CONTRY: I.S.A.
COMPUTER: ISH PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: JOCATION DATA:
APPLICATION NUMBER: US/08/159,784
FILING DATE:
APPLICATION NUMBER: US/08/159,784
FILING DATE:
APPLICATION NUMBER: S30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DECember 1, 1993
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Description of Artificial Sequence: US-09-998-831-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00246/170001
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: John F. Freeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SFSK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 SFSK 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DRAAVPIVNLKDELLFPSWEALFSGSEGFLKPGARIFSFDGKDVLRHPTWPQKSVWHGSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                   61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKFGARIFSFDGRDVLQHPAWPRKSVW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSILAGRLLEQEAASCRHAFVVLCIENSVMT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                               72 VRRADRGSVPIVNLKDEVLSPSWDSLFSGSQQQVQPGARIFSFDGRDVLRHPAWPQKSVW 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 DFQLVIHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DEGEVIALIVALNISPLSGGWRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSIVRRA
                                                                                                                                                                                                                                                                                                                                                        12 HTHQDFQPVLHLVALNTPLSGGMRGIRGADFQCFQQARAVGLSGTFRAFLSSRLQDLYSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09315689

Patent No. 6346510

GENERAL INFORMATION:
APPLICANT: Folkman, Judah
APPLICANT: Folkman, Judah
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0229
CURRENT APPLICATION UNBER: US/09/315,689
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                 1 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFOCARAAGLAGTFRAFLSSRLQDLYSI
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84.6%; Score 817; DB 4;
Best Local Similarity 85.9%; Pred. No. 1.2e-93;
Matches 152; Conservative 12; Mismatches 13
                                                                                                                                                                                                                                          Query Match 85.7%; Score 828; DB 1;
Best Local Similarity 83.2%; Pred. No. 5.8e-95;
Matches 153; Conservative 18; Mismatches 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36, Application US/08985526; Patent No. 6080728; General INFORMATION: APPLICANT: Mixson, James A
; INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-09-315-689-5
                                                                                                                                ; TYPE: amino acid
; STRANDEDNESS: N/P
; TOPOLOGY: N/A
US-08-159-784-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 SFSK 184
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US-08-985-526-36
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LENGTH: 17
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us-09-938-391-4.rai

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TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
CITY: Wilmington
STREET: 1200 Market Street, P.O. Box 2207
CITY: Wilmington
STREET: 1200 Market Street, P.O. Box 2207
COUNTER READABLE FORM:
MEDIUM TYPE: PLOSPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOSPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOSPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOSPY disk
COMPUTER: LEW PC Compatible
OPERATION SYSTEM PC-0008/MS-DOS
SOFTWARE: PARENTH RE-1009/MS-DOS
SOFTWARE: PARENTH RE-1009/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE: 16-JUL-1996
APPLICATION NUMBER: US/08/985,526
FILING DATE: 16-JUL-1996
APPLICATION NUMBER: US/08/985,526
FILING DATE: 16-JUL-1996
APPLICATION NUMBER: US/08/985,526
FILING DATE: 16-JUL-1996
APPLICATION NUMBER: US/08/985,526
APPLICATION NUMBER: US/08/985,526
APPLICATION NUMBER: US/08/68-5613
INPORATION FOR SEQ ID No: 36:
BENGTH: 185 amino acid
TOPEL: ALDOLOGY: Linear
US-08-985-526-36
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61 VRRADRIGVPVV-NLRDEVLFPSWEALFSGSEGQLKFGARIFSFDGRDVLQHPAWPRKSV 119 61 VRRADRGSVPIVQNLRDEVLSPSWDSLFSGSQGQLQPGARIFSFDGRDVLRHPAWPQRSV 120 9 9 1 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFQOARAAGLAGTFRAFLSSRLQDLYSI 2 HTHQDFQPVLHLVALNTPLSGGMRGIRGADFQCFNNAR-VGLSGTFRAFLSSKLQDLXSI Query Match
Best Local Similarity 81.1%; Pred. No. 2.9e-90;
Matches 150; Conservative 16; Mismatches 17; Indels ò 셤 ò g ò g

2; Gaps

TSFSR 185

180 TSFSK 184

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Search completed: March 26, 2004, 13:39:22 Job time : 14.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 26, 2004, 13:33:07; Search time 12.4444 Seconds (without alignments) 1422.260 Million cell updates/sec Run on:

US-09-938-391-4 966 1 HTHQDFQLVLHLVALNSPQF......CRHAFVVLCIENSVMTSFSK 184 Title: Perfect score: Sequence:

Scoring table:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMENTES Re

	Description	collagen alpha 1 (X	lagen	llagen	alpha 1	pothetical pro	Д	otei	ú	Vqr	probable Vgr prote	ginine A	ved.	٠		hypothetical prote	sulfolipid biosynt	ä	bio	ratas	probable Rhs acces	4	l pro	Beri	hs	e)	13	ne	ase	exopolyphosphatase
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	esult No.	-	7	m	4	Ŋ	ø	7	c c	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

exopolyphosphatase	exopolyphosphatase	VgrE protein [imbo	Rhs element associ	hypothetical prote	class I cytokinase	probable deaminase	beta-glucosidases	ycdS protein precu	probable outer mem	probable outer mem	58K membrane-assoc	glutamine syntheta	hypothetical prote	ಗ	hypothetical prote
D91049	H85893	D90886	B85732	A69177	JW0047	H95857	AG1662	F64844	F90787	F85647	A53798	H83944	G87687	G87369	E97241
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513	513	702	714	126	636	437	723	807	807	807	427	449	966	510	286
7.8	7.8	7.7	7.7	7.7	7.7	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.5	7.5
75.5		74.5		74	74	73.5	73.5	73.5	73.5	73.5	73	73	73	72.5	72
30	31	35	33	34	32	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

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Matches 154; Conservative
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A, Molecule type: manA

A, Rolecule type: manA

A, Rolecule type: manA

A, Rolecule type: manA

A, Rolecules type: manA

A, Cross-references: EMB1:122545; NID:9348968; PIDN:AA19787.1; PID:9511298

R; Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 4229-4233, 1994

A; Title: Isolation and sequencing of cDNAs for proteins with multiple domains of Gly-Xaa

A; Reference number: A58370; MUID:94240111; PMID:8183893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Molecule type: protein
A, Reladues: 1591-1610 - ORB>
A, Residues: 1591-1610 - ORB>
A, Reperimental source: hemangioendothelium cells
A, Note: inhibits endothelial cell proliferation
C, Comment: Prolines and lysines at the third position of the tripeptide repeating unit (ated and subsequently 0-glycosylated.
C, Comment: The different splice forms of collagen alpha 1(XVIII) may be involved in peri
                                                                                                                                                                                                                                                                           collagen alpha 1(XVIII) chain precursor, long splice form - mouse
N;Conteains: collagen alpha 1(XVIII) chain precursor, medium splice form; endostatin
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Oct-1995 #sequence_revision 08-May-1998 #text_change 15-Sep-2003
C;Accession: BSS101, C56101; S72450; S65595; PN0675; A54072; A58816
S;Rehn, M.; Pihlajaniemi, T.
J. Biol. Chem. 270, 4705-4711, 1995
A;Title: Identification of three N-terminal ends of type XVIII collagen chains and tissu
A;Reference number: A56101; MUID:95181468; PMID:7876242
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A; Cross-references: EMBL:L22545
R; Abe, N.; Muragaki, Y.; Yoshioka, H.; Inoue, H.; Ninomiya, Y.
Biochem. Biophys, Res. Commun. 196, 576-582, 1993
A; Title: Identification of a novel collagen chain represented by extensive interruptions A; Reference number: PN0675; MUID:94059075; PMID:8240330
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A;Residues: 635-1774 <ABE>
R;Rehn, M.; Hintikka, B.; Pihlajaniemi, T.
J. Biol. Chem. 269, 13929-13935, 1994
A;Title: Primary structure of the alphal chain of mouse type XVIII collagen, partial str
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A, Readudes: 1293-1403, 78, 1405-1774 < REH3>
A, Cross-references: GB: U03714; NID: 948773; PIDN: AAA20657.1; PID: 9487734
R; O'Reilly, M.S.; Boehm, T.; Shing, Y.; Fukai, N.; Vasios, G.; Lane, W.S.; Flynn, E.; Bi
Cell 89, 277-285; 1997
A; Title: Endostatin: an endogenous inhibitor of angiogenesis and tumor growth.
A; Reference number: A58816; MUID: 97160848; PMID: 9008168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: C56101
A; Molecule : 1-239, 487-52 < REH2>
A; Residues: 1-239, 487-52 < REH2>
A; Residues: 1-239, 487-52 < REH2>
A; Cross-references: GB:U11637; NID:g618429
A; Experimental source: splice form clones PE8.1, PE19, PE15.2
B; Dib, S.P; Kamagatar, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, B.R.
A; Reference to the EMBL Data Library, August 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-562 <REH1>
A;Cross-references: GB:U1637; NID:G618429; PIDN:AAC52179.1; PID:G618430
A;Experimental source: splice form clone PE17.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A54072; MUID: 94245707; PMID: 8188673
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A; Residues: 487-1512,'
        181 S 181
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Anthrone: 1295/3; 1310/1; 1345/3; 1388/3; 1437/1; 1461/3; 1505/3; 1516/3; 1595
A; Map position: 10:41.0
A; Introne: 1295/3; 1310/1; 1331/1; 1345/3; 1388/3; 1437/1; 1461/3; 1505/3; 1516/3; 1595
A; Note: the list of introne is incomplete
C; Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteogly
C; Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteogly
C; Reywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteogly
C; 1-39,487-1774/Product: collagenesis alpha 1(XVIII) chain precursor; medium splice form #status predicted <COO1-
F; 1-24/Domain: collagenesis #status predicted <COO1-
F; 122-1042/Domain: collagenesis #status predicted <COO5-
F; 1204-1042/Domain: collagenesis #status predicted <COO5-
F; 1204-1290/Domain: collagenesis #status predicted <COO5-
F; 1204-1290/Domain: collagenesis #status predicted <COO5-
F; 1216-1290/Domain: collagenesis #status predicted <COO5-
F; 1216-1290/Domain: collagenesis #status predicted <COO6-
F; 1217-1228/Domain: collagenesis #status predicted <COO5-
F; 1217-1228/Domai
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A; Residues: 1.1-03 < REN1
A; Residues: 1.1-03 < REN1
A; Residues: 1.1-03 < REN1
A; Residues: 1.1-03 < REN1
A; Residues: 1.1-03 < REN1
A; Residues: 1.1-03 < REN1
A; Reln, M.; Pihlajaniemi, T.
B; Rehn, M.; Pihlajaniemi, T.
B; Renn, M.; Pihlajaniemi, T.
B; Renn, M.; Pihlajaniemi, T.
B; Residues: Abinal (XVIII), a collagen chain with frequent interruptions in the collagenous A; Reference number: A58371; MUID: 94240112; PMID: 8183894
A; Recession: A58371
A; Molecule type: mRNA
A; Residues: 1-928 < REH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicontains : endostarin.
Nicontains : endostarin.
CiSpecies: Mus musculus (house mouse)
CiDate: Mus musculus (house mouse)
CiDate: 03-0ct-1995 #sequence_revision 08-May-1998 #text_change 15-Sep-2003
CiAccession: A56101; A56371; 572450; S65595
R;Rehn, M.; Pihlajaniemi, T.
J. Biol. Chem. 270, 4705-4711, 1995
A;Tible: Identification of three N-terminal ends of type XVIII collagen chains and tiss tif homologous to rat and Drosophila frizzled proteins.
A;Reference number: A56101; MUID:95181468; PMID:7876242
C;Comment: Endostatin is released from collagen alpha 1(XVIII) chain by the action of ay be useful in treating solid tumors. C;Genetics:
A;Gene: MGI:Collaal
A;Cross-references: MGI:71175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1591 HTHQDFQPVLHLVALNTPLSGGMRGIRGADFQCFQQARAVGLSGTFRAFLSSRLQDLYSI 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VRRADRTGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collagen alpha 1(XVIII) chain precursor, short splice form - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.0%; Score 831; DB 2; Length 1774; 83.7%; Pred. No. 3.8e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
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Apacession: A53317
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: 1-138 KKIV>
A; Cross-references: GB:L25280
A; Cross-references: GB:L25280
A; Muragaki, Y:, Abe, N.; Minomiya, Y.; Olsen, B.R.; Ooshima, A.
Biol. Chem. 269, 4042-4046, 1994
A; Title: The human alphal(XV) collagen chain contains a large amino-terminal non-triple
A; Reference number: A53146; MUID:94140817; PMID:8307960
A; Accession: A53146
A; Reference number: A53146; MUID:94140817; PMID:8307960
A; Reference contains a large amino-terminal non-triple
A; Reference contains and A; Reference contains a large amino-terminal non-triple
A; Reference contains and A; Reference contains a large amino-terminal non-triple
A; Reference contains and A; Reference contains a large amino-terminal non-triple
A; Reference contains and A; Reference contains a large amino-terminal non-triple
A; Reference contains a previously unknown human collagen chain, alphal(XV), chara
A; Reference number: S28778; MUID:93066196; PMID:1279671
A; Reference number: S28778; MUID:93066196; PMID:1279671
A; Reference contains a preliminary
A; Molecule type: mRNA
A; Reference contains a large amino-triple
A; Reference contains a large amino-triple
A; Reference contains a large amino-triple
A; Reference contains a large amino-triple
A; Reference contains a large amino-triple
A; Reference contains a large amino-triple
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A; Reference contains a large amino-triple
A; Reference contains 
C;Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text_change 15-Sep-2003
C;Accession: A53317; A53146; S28778
R;Kivirikko, S.; Heinaemeeki, P.; Rehn, M.; Honkanen, N.; Myers, J.C.; Pihlajaniemi, T. Biol. Chem. 269, 4773-4779, 1994
A;Title: Primary structure of the alphal chain of human type XV collagen and exon-intro
A;Reference number: A53317; MUID:94148920; PMID:8106446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1218 LHLAALNMPFSGDIR----ADFQCFKQARAAGLLSTYRAFLSSHLQDLSTIVRKAERYSL 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Residues: 1-650 <WIL>
A,Residues: 1-650 <WIL>
A,Cross-references: EMBL:281079; PIDN:CAB03084.1; GSPDB:GN00019; CESP:F39H11.4
A,Experimental source: clone F39H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
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CjSpecies: Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
CjAccession: T22002
RjWhite, S.
ByWhite, S.
ByWhite, S.
ByWhite, S.
ByReference number: Z19500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 PVVNLRDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDFSGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 LTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMTSFSK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross references: GDB:132578; OMIM:120325
A;Map position: 9421-9422
F;1-227Domain: signal sequence #status predicted <SIG>F:1-227Domain: signal sequence #status predicted <MAT>F:23-1388/Product: collagen alpha 1(XV) chain #status predicted <MAT>F;1216-1388/Region: multiplexin collagen carboxyl-terminal homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 1
A;Introns: 109/3; 154/1; 357/1; 420/3; 464/3; 566/2; 594/1; 628/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.5%; Score 526; DB 2; Length 13 56.6%; Pred. No. 2.8e-43; ative 27; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Status: preliminary, translated from GB/EMBL/DDBJ A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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A;Gene: CESP:F39H11.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Gene: GDB:COL15A1
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 28-687, L', 689-734,'F',736-751,'R',753-1315 <OHW>
A;Residues: 28-687,'L', 689-734,'F',736-751,'R',753-1315 <OHW>
A;Cross-references: EMBL:L22545, MID:9348968; PIDN:AAA19787.1; PID:9511298
B;Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 4229-4233, 1994
A;Title: Isolation and sequencing of cDNAs for proteins with multiple domains of Gly-Xaa
A;Reference number: A58370; MUID:94240111; PMID:8183893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 28-1315 <OHS>
A; Residues: 28-1315 <OHS>
A; Residues: 28-1315 <OHS>
A; Cross-references: BMBL:L22545
C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C; Comment: Prolines and Subsequently O-glycosylated.
C; Comment: The different splice forms of collagen alpha 1(XVIII) may be involved in perificomment: The different splice forms of collagen alpha 1(XVIII) chain by the action of unity be useful in treating solid tumors.
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Fill3-1315/Product: endostatin #status predicted <EST>
Fill39-1315/Product: endostatin collagen carboxyl-terminal homologous
Fill26,488/Bainding site: carbotydrate (Asn) (covalent) #status predicted
Fill20-228/Disulfide bonds: #status predicted
Fill240,245,1257/Binding site: carbotydrate (Ser) (covalent) #status predicted
Fi451,454,594/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
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                            A,Cross-references: GB:L16898; NID:g404754; PIDN:AAA37434.1; PID:g553894 R;Oh, S.P.; Kamagatea, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, B.R. submitted to the EMBL Data Library, August 1993 A;Reference number: S72450
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; Pred. No. 5.2e-73;
18; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A53317
collagen alpha 1(XV) chain precursor - human
N'Alternate names: procollagen alpha 1(XV) chain
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.7%;
83.2%;
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Best Local Similarity
Matches 153; Conserv
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A;Residues: 1-995 cRHO> A;Cross-references: GB:NP_443083; PID:g16445031; PIDN:NP_443083.1 Query Match Best Local Similarity 23.0%; Pred. No. 8.9; Best Local Similarity 23.0%; Pred. No. 8.9; Matches 37; Conservative 26; Mismatches 52; Indels 46; Gaps 7; Qy 52 SRLQDLYSIVRRADRTGVPVVNLRDEVLFPSWEALFSGSEGGLKPG 97 Qy 52 SRLQDLYSIVRRADRTGVP	RESULT 8 T36950 Probable transcription regulator - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #totales comparing to the EMBL Date Library, September 1999 R;Secent C to the EMBL Date Library, September 1999 A;Reference number: Z21607 A;Accession: T36950 A;Accession: T36950 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-190 <ser> A;Accession: T600 <serpe: <<="" <serpe:="" t600="" th=""><th>Query Match Best Local Similarity 25.1%; Pred, No. 1.4; Matches 46; Conservative 18; Mismatches 60; Indels 59; Gaps 10; Matches 46; Conservative 18; Mismatches 60; Indels 59; Gaps 10; QY 11 HIVALNSPQPGGMRGADF</th><th>RESULT 9 goodale Vgr protein [imported] - Bscherichia coli (strain O157:H7, substrain RIMD 050' C;Species: Bscherichia coli C;Species: Bscherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: G90704 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C (gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ger A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: G90704 A;Accession: G90704 A;Accession: G90704 A;Molecule type: DNA</th></serpe:></ser></ser></ser></ser></ser></ser></ser></ser></ser></ser></ser></ser></ser>	Query Match Best Local Similarity 25.1%; Pred, No. 1.4; Matches 46; Conservative 18; Mismatches 60; Indels 59; Gaps 10; Matches 46; Conservative 18; Mismatches 60; Indels 59; Gaps 10; QY 11 HIVALNSPQPGGMRGADF	RESULT 9 goodale Vgr protein [imported] - Bscherichia coli (strain O157:H7, substrain RIMD 050' C;Species: Bscherichia coli C;Species: Bscherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: G90704 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C (gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ger A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: G90704 A;Accession: G90704 A;Accession: G90704 A;Molecule type: DNA
Ouery Match 37.9%; Score 366; DB 2; Length 650; Best Local Similarity 44.1%; Pred. No. 6.2e-28; Matches 75; Conservative 26; Mismatches 63; Indels 6; Gaps 4; Qy 9 VLHIVALNSPOPGOMERAGE COPROLATERELSSRLODLYSIVERDRIG 68 1	AB3204 AB3204 AB3204 AB3204 AB3204 AB3204 C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Accession: A83204 AGanan, S; Yuan, X; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradan, S; Yuan, Y; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lian, J. Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Accession: A83204 A;Accession: A832104 A;Access	Ouery Match Query Match Best Local Similarity 24.6%; Score 87; DB 2; Length 494; Best Local Similarity 24.6%; Pred. No. 1.2; Matches 45; Conservative 20; Mismatches 68; Indels 50; Gaps 7; Qy 4 QDFQLVLHLVALNSPQPGGGRGADFF	RESULT 7 H59432 RhoGAP protein homolog [imported] - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: H5943 S;Rhodes, S: Submitted to GenBank, October 2001 A;Pescription: Novel human gene mapping to chomosome 13, similar to rat RhoGAP. A;Reference number: H59432 A;Accession: H59432 A;Status: preliminary A;Molecule type: DNA

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A;Molecule type: DNA
A;Residues: 1-346 <STO>
A;Residues: 1-346 <STO>
A;Cross-references: GB:AE004831; GB:AE004091; NID:g9950347; PIDN:AAG07536.1; GSPDB:GN00
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 V---VNLRDEVLFPSWEALFSG----SEGOLKPG-----ARIFSFDGRDVLQHPAWP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 MRLHPDARESLLVPLAPGLLVGCGVSAAGYLOPGVAHAPSLSSGTLALDGEREIEFSATD 308
                                                                                                                                                                                                                                                                                                       128 SHQDYIHSYHFKTLHFFLTQALFALRASQPRCYYVYRGVRGIR-----FMTQR--GKSV 179
                                                                                                                                                                                                                                                                                                                                                                                                              180 RFGQFTSTSLRKEATVNFGQDTLFVVKTC--YGVPIKQFSFFPSEDEVLIPPFEVFEVIN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LKPGARIFSFDGRDV-----LQHPAWP-RKSVW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 FSNDRGSVKIQLHSKGKMSTHNCELLKPQGGQWGRGHQEVGLGLSPGLSLPVLPCRRRVW 297
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                                                                                                                                                                                                                                                                                                                                                                   TFRAFLSSRL-----QDLYSIVRRADRIGVPVVNL----RDEVLFPSWEAL---- 86
                                                                                                                                                                                                                                                2 THOD------FQLVLHLVALNSPQP-----GGNRGIRGADFQCFQQARAAGLAG
A, Residues: 1-312 <TSU>
A, Residues: 1-312 <TSU>
A, Cross-references: GB: D31864; NID: g1638784; PIDN: BAA06664.1; PID: g1638785
C; Superfamily: NAD(P) +-arginine ADP-ribosyltransferase
C; Keywords: g1ycosyltransferase; NAD; pentosyltransferase
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                                                                                                                                  Query Match
8.4%; Score 81; DB 2; Length 312;
Best Local Similarity 26.3%; Pred. No. 2.8;
Matches 50; Conservative 13; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 RPSI--TLDPSG------PFSVDVPATLAYAARHRLLAGQ 340
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8.2%; Score 79.5; DB 2;

Best Local Similarity 27.6%; Pred. No. 4.4;

Matches 45; Conservative 19; Mismatches 56;
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 23-Nar-1995 #sequence_revision 23-Mar-1995 #text_change 03-Jun-2002
C;Accession: A55461
R;Tsuchiya, M.; Hara, N.; Yamada, K.; Osago, H.; Shimoyama, M.
A;Title: Chem. 256; 27451-27457, 1994
A;Title: Cloning and expression of cDNA for arginine-specific ADP-ribosyltransferase frc
A;Reference number: A55461
A;Accession: A55461
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable vgr protein [imported] - Escherichia coli (strain 0157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001
C;Accession: B85555
C;Pate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001
C;Date: 16-Feb-2001 #sequence 0.3.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
A;Reference number: A88480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005174; NID:g12513451; PIDN:AAG54902.1; GSPDB:GN00145; UMGP:207
A;Experimental source: strain 0157:H7; substrain EDL933
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8.4%; Score 81.5; DB 2; Length 633;
Best Local Similarity 24.4%; Pred. No. 5.8;
Matches 40; Conservative 18; Mismatches 59; Indels 4
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8.4%; Score 81.5; DB 2;
Best Local Similarity 24.4%; Pred. No. 5.8;
Matches 40; Conservative 18; Mismatches 59;
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A,Molecule type: DNA
A,Residues: 1-633 <STO>
         A;Residues: 1-633 <HAY>
                                                                                                                      A;Gene: ECs0607
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A;Accession: D90658
A;Accession: preliminary
A;Residues: preliminary
A;Residues: 1-713 cHAY>
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC50236
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R. Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
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8.2%; Score 79.5; DB 2; Length 713;
Best Local Similarity 24.4%; Pred. No. 10;
Matches 40; Conservative 18; Mismatches 59; Indels 47;
                                                                                                                                                                                                        59; Indels 47;
                                                                                                                                                                       Length 713;
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                                                                                                                                                                                                                                                                                                                     DB 2;
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8.2%; Score 79.5; Di
Best Local Similarity 24.4%; Pred. No. 10;
Matches 40; Conservative 18; Mismatches
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A,Reference number: 221596
A,Accession: T36083
A,Status: pre-liminary;
A,Status: pre-liminary;
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-672 <8AU>
A,COSS-references: EMBL,AL049661; PIDN:CAB41199.1; GSPDB:GN00070; SCOEDB:SCE134.01c
A,Experimental source: strain A3(2)
C,Genetics:
A,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                              48 AFLSSRIQDLYSIVRRADRIGVPVVNLRDBYLFPSWEALFSGSEGQLKPGARIFSFDGRD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                  108 VLQHPAWPRKSVWHGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRH 167
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8.2%; Score 79; DB 2;
Best Local Similarity 31.5%; Pred. No. 11;
Matches 39; Conservative 10; Mismatches 3;
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P39060 homo sapien
P39061 mus musculu
P39053 homo sapien
P55678 gallus gall
Q973m8 homo sapien
Q14957 homo sapien
P55806 gallus gall
P31521 pseudomonas
Q8bbb0 mus musculu
P59641 h replicase
P29014 escherichia
Q9126 homo sapien
P7507 escherichia
Q9126 homo sapien
P45476 escherichia
Q9126 homo sapien
P45476 escherichia
Q9126 foresphila
Q9129 qarlus gall
Q82169 rattus norv
Q92080 gallus gall
P55807 gallus gall
Q8216 streptomyce
P1329 european el
P1329 european el
P1329 european el
P1329 musculu
Q9210 streptomyce
P1537 mus musculu
O950144 rattus norv
P58750 mus musculu
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O97644 rattus norv
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O97644 rattus norv
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                                                                                                        March 26, 2004, 13:29:16; Search time 9:33333 Seconds (without alignments) 1026.526 Million cell updates/sec
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1 HTHQDFQLVLHLVALNSPQP......CRHAFVVLCIENSVMTSFSK 184
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

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e e	HUMAN STANDARD;
A C	P39060; Q9UK38; Q9Y6Q7; Q9Y6Q8; 01-FRR-1995 (Rel. 31. Created)
拮	16-OCT-2001 (Rel. 40, Last sequence update)
E E	15-MAR-2004 (Rel. 43, Last annotation update) מבוויה ביווף (איוד אחלה ביווף) באינים האיפורים (Contains: Endostatin)
3 Z	Precuise Comments
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RP	SEQUENCE FROM N.A.
X 6	MEDLINE=98164096; PubMed=9503365;
5 E	orma
E	ences in the
RT	corresponding transcripts.";
R.	Matrix Biol. 16:319-328(1998).
2 G	[2] I WOOD DOWN N A
×	MEDI.TNE=20289799: PubMed=10830953:
Z Z	Hattori M. Fulivama A., Taylor T.D., Watanabe H., Yada T.,
Æ	Park HS., Toyoda A., Ishii K., Totoki Y., Choi DK., Groner Y.,
R.	Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
R.A	Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
ξ.	Reichwald K., Kump A., Schlinbel M., Schudy A., Limmer M.,
8 :	Roberthal A., Kudon J., Shilbuya K., Kawatakir A., Asakawa J., Alamanakir A., Asakawa J., A., A., A., A., A., A., A., A., A., A
ξ d Δ	Shincani A., Sasaki I., Nagamine N., Mitsuyama S., Mitsuyama S., Mitsuyama S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
5 4	Acharfe M. Schoen O. Desario A. Reichelt J., Kauer G., Bloecker H.
5 5	A Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
R.	Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
R.A	Lehrach H., Reinhardt R., Yaspo ML.;
RI.	"The DNA sequence of human chromosome 21.";
7 Z	Macure 403:311-313(4000/:
2 G	SEQUENCE OF 834-1516 FROM N.A.
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RA	Oh S.P., Warman M.L., Seldin M.F., Cheng S., Kholl J.H., Timmons S.,
R E	Olsen B.R.; "Closian of apm and cenomic DMs encoding human fone XVIII collagen
7 E	II) collagen gene to mou
E.	lan chromosome 21.";
짚	:494-499 (1994
Z :	[4]
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) A	o L., Wei-Jie Z., Xiang-Fu W.;
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RP	INVOLVEMENT IN KNOBLOCH SYNDROME.

'roDom; PD000007; Clg_helix; 1.

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RED MINE-215:8361; PubMed-11608364;

RED MINE-216:8361; PubMed-11608364;

Red Mine-216936; PubMed-1160836;

Red Mine-216936;

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EMBL; AP018082; BAC39659.1; -
EMBL; AL16302; CAB90482.1; -
EMBL; L22548; AA51864.1; -
EMBL; AL18408; AAF51864.1; -
EMBL; D22548; AAF5180.1; ALT_INIT.
PDB; 13NL; 02-DEC-98.
Ganew; HGMC:2195; COL18A1.
MIM; 120328; -
MIM; 20328; -
MIM; 203750; -
MEDLINE=20400145; PubMed=10942434; Seria M., Brahe C., Seria B., Containing A.A., Zatz M., Brahe C., Seria V., Camargo A.A., Zatz M., Brahe C., Sossi V., Camargo A.A., Zatz M., Brahe C., Collagen M.R.; Collagen XVIII, containing an endogenous inhibitor of angiogenesis and tumor growth, Jays a critical role in the maintenance of retinal structure and in neural tube closure."; Hum. Mol. Genet. 9:2051-2058(2000).
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GO; GO:0005581; C:collagen, TAS.

GO; GO:0008282; P:negative regulation of cell proliferation, TAS.

GO; GO:00080601; P:vision; TAS.

InterPro; IPRO08161; Clg helix.

InterPro; IPRO08162; ConA like lec_gl.

InterPro; IPRO08985; ConA like lec_gl.

InterPro; IPRO08129; TSPN.

InterPro; IPRO08129; TSPN.

Pfam; PF01391; Collagen; 7.

Pfam; PF01301; Collagen; 7.
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COLLAGEN ALPHA 1 (XVIII) CHAIN.
ENDOSTATIN.
TSP N-TERMINAL.
NONHELICAL REGION 1 (NC1).
TRIPLE-HELICAL REGION 2 (NC2).
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          SMART; SM00282; Land; 1.
SMART; SM00282; Land; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Glycoprotein; Signal; Alternative splicing;
Polymorphism; 3D-structure.
1 23 POTENTIAL.
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tive 14; Mismatches 13; Indels C
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        61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120
                                                                                                                                                              121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180
1 HTHODFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI
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MEDLINE-94240111; PubMed-8183893;
Ob S.P., Kamagata Y., Muragaki Y., Timmons S., Ooshima A., Olsen B.R.;
"Isolation and sequencing of cDNAs for proteins with multiple domains of Gly-Xaa-Yaa repeats identify a distinct family of collagenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECURNCE FROM N.A. (ISOFORM 3).
STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=94245707; PubMed=8188673;
Rebln M.V., Hintikka E., Pihlajaniemi T.;
Rehm M.V., Hintikka E., Pihlajaniemi T.;
Primary structure of the alpha 1 chain of mouse type XVIII collagen,
partial structure of the corresponding gene, and comparison of the
alpha 1 (XVIII) chain with its homologue, the alpha 1 (XV) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE OF 1-1387 FROM N.A. (ISOFORM 3).
MEDIATRE-84-840112; PubMed=8183894;
READA M.V., Pihlajaniemi T. PubMed=8183894;
"Alpha 1(XVIII), a collagen chain with frequent interruptions in the collagenous sequence, a distinct tissue distribution, and homology with type XV collagen.";
Proc. Natl. Acad. Sci. U.S.A. 91:4234-4238(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1591-1774 FROM N.A.
MEDLINE=11217748; PubMed=11321448;
Jia S., Zhu F., Li H., He F., Xiu R.-J.;
"Anticancer treatment of endostatin gene therapy by targeting tumor neovasculature in C57/BL mice.";
Clin. Hemorheol. Microcirc. 23:251-257(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITINE-96435922; PubMed-8838808; Rehn M., Hintikka E., Pihlajaniemi T.; Characterization of the mouse gene for the alpha-1 chain of type XVIII collagen (COLL8A1) reveals that the three variant N-terminal polypeptide forms are transcribed from two widely separated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                           CAIH MOUSE STANDARD; PRT; 1774 AA.
P39061; 060672; 061437; 062001; 062002; 094763;
01-FEB-1995 (Rel. 31, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Collagen alpha 1(XVIII) chain precursor [Contains: Endostatin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 91:4229-4233(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 269:13929-13935(1994).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Blioinformatics and the FNBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELE-ALITATIVE SPLICE.

C Name=1; Synonyms=NO1-61; Sequence=Displayed;

I soId=P39061-3; Sequence=Displayed;

C Name=2; Synonyms=Long, NO1-517;

C Note=produced by alternative splicing of isoform 1;

Note=produced by alternative splicing of the tripeptide repeating;

C Name=3; Synonyms=Short, NO1-301;

I soId=P39061-2; Sequence=VSP 001157, VSP 001158;

C -!- PTM: Prolines at the third position of the tripeptide repeating

C -!- PTM: Prolines at the third position of the tripeptide repeating

C -!- PTM: Prolines at the third position of the tripeptide repeating

C -!- SIMILARITY: Contains I FIRRIL-ASSOCIATED COLLAGENS WITH

INTERRUPTED HELICES (PROLIT) PAMILY.

C -!- SIMILARITY: Contains I fizzled (FZ) domain.
                                                                                                                                                                                                                                                                                               MEDLINE-98169382; PubMed-9501087;
Hohenester E., Sasaki T., Olsen B.R., Timpl R.;
"Crystal structure of the anglogenesis inhibitor endostatin at 1.5-A
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO J. 17:1656-1664(1998).

-!- FUNCTION: Endobstatin potently inhibits endothelial cell

-!- PUNCTION: Endobstatin potently inhibit angiogenesis by
pinding to the heparan sulfate proteoglycans involved in growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative promoter;
Comment=2 isoforms, 1 (shown here) and 3, are produced by use
of alternative promoters;
Event=Alternative splicing; Named isoforms=3;
CHARACTERIZATION OF ENDOSTATIN, AND PARTIAL SEQUENCE.
MEDLINE=97160848; PubMed=9008168;
O'Reilly M.S., Boehm T., Shing Y., Fukai N., Vasios G., Lane W.:
Flynn E., Birkhead J.R., Olsen B.R., Folkman J.;
"Endostatin: an endogenous inhibitor of angiogenesis and tumor
                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF ENDOSTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 116898; AAA37434.1; ---
EMBL; U03714; AAA20657.1; ---
EMBL; U34606; AAC52901.1; JOINED.
EMBL; U34608; AAC52901.1; JOINED.
EMBL; U34609; AAC52901.1; JOINED.
EMBL; U34610; AAC52901.1; JOINED.
EMBL; U34610; AAC52901.1; JOINED.
EMBL; U34611; AAC52901.1; JOINED.
EMBL; U34612; AAC52901.1; JOINED.
EMBL; U34613; AAC52901.1; JOINED.
EMBL; U03716; AAC52901.1; JOINED.
EMBL; U03716; AAC52901.1; JOINED.
EMBL; U03718; AAC52901.1; JOINED.
EMBL; U03718; AAC52901.1; JOINED.
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AAC52902.1;
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U34608; AAC52903.1;
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Firid-USP 001157.
AGDRLPVVCÄSLPSQEDGYCVFIGPAA -> MAPRWHILDV
LTSLVLILVARVSWARP (in isoform 3).
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TRIPLE-HELICAL REGION 1 (COL1).
NONHELICAL REGION 2 (NC2).
TRIPLE-HELICAL REGION 3 (COL2).
NONHELICAL REGION 3 (NC3).
TRIPLE-HELICAL REGION 4 (NC4).
TRIPLE-HELICAL REGION 4 (COL4).
NONHELICAL REGION 4 (COL4).
TRIPLE-HELICAL REGION 5 (COL5).
TRIPLE-HELICAL REGION 6 (NC6).
TRIPLE-HELICAL REGION 6 (NC6).
TRIPLE-HELICAL REGION 7 (NC7).
TRIPLE-HELICAL REGION 7 (NC7).
TRIPLE-HELICAL REGION 7 (NC7).
NONHELICAL REGION 9 (COL9).
NONHELICAL REGION 10 (NC1).
TRIPLE-HELICAL REGION 10 (NC1).
NONHELICAL REGION 10 (NC1).
TRIPLE-HELICAL REGION 10 (COL10).
NONHELICAL REGION 11 (NC11).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
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P -> L (IN REF. 4).
P -> F (IN REF. 4).
A -> R (IN REF. 4).
EMBL; U34609; AACS2903.1; JOINED.
EMBL; U34610; AACS2903.1; JOINED.
EMBL; U34611; AACS2903.1; JOINED.
EMBL; U34612; AACS2903.1; JOINED.
EMBL; U34613; AACS2903.1; JOINED.
EMBL; U3163; AACS2178.1; ---
EMBL; U21637; AACS2178.1; ---
EMBL; L22545; AAALS19787.1; ---
EMBL; AZS57775; AAF69009.1; ---
EMBL; AS6101; AS6101
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                              1651 VRRADRGSVPIVNLKDEVLSPSWDSLFSGSQQQLQPGARIFSFDGRDVLRHPAWPQKSVW 1710
                                                                                                                                                                                                                                                                              61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLOHPAWPRKSVW 120
                                                                                                                                                                                                                                                         121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180
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                                                                                                                1591 HTHODFOPVLHLVALNTPLSGGMRGIRGADFOCFOQARAVGLSGTFRAFLSSRLQDLYSI
                                                                                    1 HTHODFOLVLHLVALMSPOPGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLODLYSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primary structure of the alpha 1 chain of human type XV collagen and exon-intron organization in the 3' region of the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
MEDLINE=94140817, PubMed=8307960;
MEDLINE=94140817, PubMed=8307960;
MILTENE=94140817, PubMed=8307960;
The human alpha 1(XV) collagen chain contains a large amino-terminal non-triple helical domain with a tandem repeat structure and homology to alpha 1(XVIII) collagen.";
To alpha 1(XVIII) collagen.";
J. Biol. Chem. 269:4042-4046(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 544-1252 FROM N.A.
MEDLINE-93066196; PubMed=1279671;
Myers J.C., Kivirikko S., Gordon M.K., Dion A.S., Pihlajaniemi T.;
Myers J.C., Kivirikko S., Gordon M.K., Dion A.S., Pihlajaniemi T.;
Identification of a previously unknown human collagen chain, alpha
"[KV), characterized by extensive interruptions in the triple-helical
region.";
                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 89:10144-10148 (1992).

-I TISSUE SPECIFICITY: Expressed predominantly in internal organs such as drenal gland, pancreas and kidney.

-I PTM: Prollines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.

-I SIMILARITY: BELONGS TO THE FIRSTL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) PAMILY.

-I SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUB-Umbilical cord;
MEDLINE-94148920; PubMed=8106446;
KYVITIKKO S., Heinamaki P., Rehn M.V., Honkanen N., Myers J.C.,
Pihlajaniemi T.;
Query Match
86.0%; Score 811; DB 1; Length 1774;
Best Local Similarity 83.7%; Pred. No. 6.4e-72;
Matches 154; Conservative 17; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
COllagen alpha 1(XV) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene.";
J. Biol. Chem. 269:4773-4779(1994).
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  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PP0210; TSPN; 1.
SNART; SN00282; Land; 1.
SNART; SN00210; TSPN; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cellagen; Glycoprotein; Signal.
SIGNAL
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(NC3).
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                                                                                                                                                                                                                                                                   COLLAGEN ALPHA 1 (XV) CHAIN.
TEP N-TERMINAL.
TONNHELICAL REGION 1 (NC1).
TRIPLE-HELICAL REGION 2 (NC2).
NONHELICAL REGION 2 (NC2).
NONHELICAL REGION 3 (NC3).
TRIPLE-HELICAL REGION 3 (NC3).
TRIPLE-HELICAL REGION 3 (NC3).
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(COL7).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NONHELICAL REGION 7 (NC7).
TRIPLE-HELICAL REGION 7 (COL7).
NONHELICAL REGION 8 (NC8).
TRIPLE-HELICAL REGION 8 (COL8).
NONHELICAL REGION 9 (NC9).
                                                                                                                                                                                                                                                                                                                                                                               (COL4)
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49 D -> V (IN REF. 2).
55 L -> A (IN REF. 2).
150 P -> A (IN REF. 2).
204 M -> V (IN REF. 2).
409 R -> A (IN REF. 2).
409 R -> A (IN REF. 2).
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NONHELICAL REGION 10 (NC10)
4 X TANDEM REPEATS.
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NONHELICAL REGION 5 (NC5)
TRIPLE-HELICAL REGION 5 (
NONHELICAL REGION 6 (NC6)
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N-LINKED (GLCNAC. ..)
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                                                          EMBL; L25286; AAA58429.1; -.
EMBL; L01697; -; NOT_ANNOTATED_CDS.
PTR; A33317; A53317.
HSSP; R99061; IKOE.
Genew; HGNC:2192; COL15A1.
NTM; 120325; -.
InterPro; IPR008995; ConA_like_lec_gl.
InterPro; IPR008995; ConA_like_lec_gl.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
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                                 1334 LVDNYCEAWRTADTAVTGLASPLSTGKILDQKAYSCANRLIVLCIENSFWTDARK 1388
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130 LIDSYCETWRIEAPAAIGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMISFSK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94124011; PubMed=8294014; Maharaj R., May T.B., Wang S.-K., Chakrabarty A.M.; Sequence of the alg8 and alg44 genes involved in the synthesis of alginate by Pseudomonas aeruginosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: Alginate biosynthesis.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the glycosyltransferase family 2.
                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Transmembrane, Complete proteome.
                                                                                                                                                                                  ALGS PSEAE STANDARD; PRT; 494 AA. 052463, 091470; 10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 4LGS OR PA3541.
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494 AA; 56456 MW;
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                                                                                                  159 GTGKRDGLAYGFRAISRHLPDDDAVVAVIDGDTVLDHGVVKKTVPWFKLFPNVGGLTTNE 218
                                                                                                                                                                                           87 FSGSEGOLKPGARIFS-----FDGRDVLQHPAWPRKSVWHGSDPS-GRRLTDS 133
39 KDFILLIGAVGIWRYSMGGVHFLRGMLFLHVVYPYYRRRVRQLGSAADPSHVFLMVTSFR 98
                                                             during limb development.";

Dev. Biol. 180:273-283(1996).

-!- PUNCTION: MAY REGULATE THE TRANSCRIPTION OF SPECIFIC GENES DURING NORMAL DEVELOPMENT. MAY PLAY A ROLE IN CRANIOFACIAL DEVELOPMENT AND DIGITAL DEVELOPMENT, AS WELL AS DEVELOPMENT OF THE CENTRAL NERVOUS SYSTEM AND GASTROINTESTINAL TRACT. IMPLICATED IN THE TRANSDUCTION OF SH4 SIGNAL (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Nuclear:
-!- SIMILARITY: BELONGS TO THE GLI FAMILY OF C2H2-TYPE ZINC-FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
21nc finger protein Glil (Fragment)
Glil OR Glil
Gallus gallus (Chicken)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
PubMed=8948590;
Marigo V., Johnson R.L., Vortkamp A., Tabin C.J.;
Marigo V., Johnson R.L., Vortkamp A., Tabin C.J.;
Sonic hedgehog differentially regulates expression of GLI and GLI3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007087; Znf C2H2.
Pfam; PF00096; zf-C2H2; 5.
SMART; SM00355; ZnF C2H2; 5.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS50159; ZINC_FINGER_C2H2_2; 5.
Zinc_finger; Metal-binding; DNA-binding; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h
Similarity 26.4%; Pred. No. 1.3;
53; Conservative 20; Mismatches 75; Indels 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   556 AA
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HSSP; P08151; 2GLI.
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ZN_FING 280 307
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NCBL_TaxID=9031;
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P55878;
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Matches 53
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                                                                                                                                                                                                                                                                                  157 PPCSSHBTLSSRPGLLHPTPARGTIKHCQQLKLERSLSSPLTAKYPEB-KSEGDISSPAS 215
                                                                                                                                                                       97 QTVIRTSPNSLVAFINSRCASAGGSYGHLSISTISPSLGYQNPPGQQQKGQGQLFSHTPPL 156
                                                                                                                                                                                                                                                 103 -----FDGRDVLQHPAWPRKSVWHGSDPSGRR-----LTDSYCETWRTE----APAA 145
                                                                                                                     ---FSGSEGOLKPGARIFS---- 102
                                                        96
                                                        47 SHHGYGLV----PGTEHPGG-----AADGSRFSTPRGAGKLGKKKALSISPLSDSSVDL
THODPOLVLHLVALNSPOPGGMRGIRGADFOCFQQARAAGLAGTFRAF----LSSRLQDL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Injuditant annotation update)
28-REAR-1 lipid transfer protein 13 (StARD13) (START domain-containing protein 13) (46H23.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
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23.0%; Pred. No. 5.4;
Ive 26; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -I- FUNCTION: May function as a GTPBase-activating protein.
-I- SIMILARITY: Contains 1 Rho-GAP domain.
-I- SIMILARITY: Contains 1 START domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Khodes S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hunt A.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                            58 YSIVRRADRIGVPVVNLRDEVLFPSWEAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       995 AA
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START.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         216 †GTQDPLL-GMLSVRDDLEKE 235
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EMBL; 284483; CAC94774.1; -.
PIR; H59432; H59432.
Genew; HGNC:19164; STARD13.
InterPro; IPR008936; Rho GAP.
InterPro; IPR00198; RhoGAP.
InterPro; IPR000198; RhoGAP.
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Pfam; PF01822; STRAT; 1.
SMART; SM00324; RTART; 1.
PROSITE; PS0238; RHOGAP; 1.
PROSITE; PS5048; START; 1.
GTPade activation: 545
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Best Local Similarity 23.0%;
Matches 37; Conservative 2
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us-09-938-391-4.rsp

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------ARIFSFD----GRDVLQHPAWPRKSVWHGSDPSGRRLTDSY---CETWR 139
                                                                                                                                     96 OCCIDNPVMLDAPLVSSSLPQPPRDVLNHPFHPK-----NEKPTRARAKSFLKRMETLR 149
                           36 SRVDDLYTLLPRGDRNGSFQGTGMRNTTSSESVLTDLSEBEVCSIHSESSGGSDSRSQPG 95
-- VVNLRDEVLFPSWEALFSGSEGQLKPG 97
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  SRLQDLYSIVRRADRTGVP----
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Old957, Old-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Glutamate [NMDA] receptor subunit epsilon 3 precursor (N-methyl Daspartate receptor subtype 2C) (NR2C) (NMDAR2C). STANDARD; Homo sapiens (Human) NME3_HUMAN ID _NME3_HUMAN

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;

WEDLINE-97189248; PubMed=9037519;
WEDLINE-97189248; PubMed=9037519;
MEDLINE-97189248; PubMed=9037519;
Lin Y.J., Bovetto S., Carver J.M., Giordano T.;
Lin Y.J., Bovetto S., Carver J.M., Giordano T.;
Lin Y.J., Bovetto S., Carver J.M., Giordano T.;
Lin Y.J., Barin Res. A3:57-64(1996).
Lin Radin Res. Mol. Brain Res. 43:57-64(1996).
Lin Radin Res. Mol. Brain Res. 43:57-64(1996).
Lin FUNCTION: NMDA receptor subcype of glutamate-gated ion channels with high calcium permeability and voltage-dependent sensitivity.
Lin Radin Res. Mol. Brain Res. Composition of an epsilon subunit and a zeta subunit.
Ci. SUBGELUTAR LOCATION: Integral membrane protein.
Linsup SPECIFICITY: Mainly in brain with predominant expression is candate nucleus, corpus callosum, subchalamic nuclei and chalamus.
Composition of the heart, skeletal muscle and pancreas.
Composition of the ligand-gated innit.

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EMBL; L76224; AAA88096.1; -. HSSP; P19491; 1CR2. Genew; HGNC:4587; GRIN2C. MIM; 138254; -.

1029 YSSFPRADRSGRPFL----PLPPELEDLPLIGKEQL---AR-----REALLHAAWAR- 1073 58 YSIVRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRK 117 118 SVWHGSDPSGRRLTDSYCETWR--TEAPA-ATGQASSLLAG----RLLEQEAASCRHAFV 170 26; Gaps GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3.
1 (POTENTIAL).
2 (POTENTIAL).
4 (POTENTIAL).
4 (POTENTIAL).
FUNCTIONAL DETERMINANT OF NMDA RECEPTORS (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
Query Match 8.5%; Score 82; DB 1; Length 1233; Best Local Similarity 32.8%; Pred. No. 6.9; 9; Mismatches 49; Indels 41; Conservative 70 7 337 33 438 43 539 53 1233 AA; 1130 EACQE 1134 171 VLCIE 175 CARBOHYD CARBOHYD CARBOHYD SEQUENCE TRANSMEM TRANSMEM TRANSMEM SITE CARBOHYD TRANSMEM 쉱 ઠે g ò

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
78-FEB-2003 (Rel. 41, Last annotation update)
78-FEB-2003 (Rel. 41, Last annotation update)
78-FEB-2003 (BC)
78-FEB-20 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=White leghorn; TISSUB-Bone marrow;
MEDLINE-95050487; PubMed=7961658;
TSUCHINA M., Hara N., Yamada K., Osago H., Shimoyama M.;
"Cloning and expression of cDNA for arginine-specific ADFTiboyltransferase from chicken bone marrow cells.";
J. Biol. Chem. 269:27457(1994).
-I- CATALYTIC ACTIVITY: NAD(+) + L-arginine = nicotinamide + N(2)-(ADF-D-ribosyl)-L-arginine.
-!- SUBCELULAR LOCATION: THE MATURE ENZYME IS PROBABLY SECRETED FROM GRANULOCYTES INTO THE EXTRACELULAR SPACE.
-!- SIMILARITY: Belongs to the Arg-specific ADP-ribosyltransferase 312 AA. NCBI_TaxID=9031;

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EMBL; D31864; BAA06664.1; -. PIR; A55461; A55461. InterPro; IPR000768; ART. Pfam; PF01129; ART; 1.

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43; Conservative 26; Mismatches
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                     87 FSGSEGQ-----LQHPAMP-RXSVW 120
                                                                                                                                                                                                                                                                                                         128 SHÓDYIHSYHFKTLHFFLTQALFALRASÓÞRCYYVYRĞVRĞIR-----FMTQR--GKSV 179
                                                                                                                                                                                                                                                                                                                                                                              180 RFGQFTSTSLRKEATVNFGQDTLFVVKTC--YGVPIKQFSFFPSEDEVLIPPFEVFEVIN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 FSNDRGSVKIQLHSKGKMSTHNCELLKPQGGQWGRGHQEVGLGLSPGLSLPVLPCRRRVW 297
                                                                                                                                                                                                                                                                                                                                              45 TFRAFLSSRL-----QDLYSIVRRADRTGVPVVNL----RDEVLFPSWBAL---- 86
                                                                                                                                                                                                                                                                       2 THOD-----FOLVLHLVALNSPOP-----GGMRGIRGADFOCFOOARAAGLAG 44
                                                                                                                                                                                                                                    76; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and characterization of genes responsible for metabolism of nitrile compounds from Pseudomonas chlororaphis B23.";
J. Bacteriol. 173:2465-2472(1991).
-!- PUNCTION: THE PRESENCE OF P47K IS CRITICAL FOR THE EXPRESSION OF THE NITRILE HYDRATASE GENES. MAY STABILIZE OR ACTIVATE THE NITRILE HYDRATASE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91193202; PubMed=2013568;
Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                             Query Match.

8.4%; Score 81; DB 1; Length 312;
Best Local Similarity 26.3%; Pred. No. 1.8;
Matches 50; Conservative 13; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.0%; Score 77; DB 1; Length 419; 24.0%; Pred. No. 6.1;
     PAINLS, FACOTOS, ART, 1.
Transferase, Glycosyltransferase, NAD, Signal, Zymogen.
Transferase, 1
20
POTENTIAL.
                                                                                                                                                             312 AA; 35318 MW; B82980439BC904FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46666 MW; FF5113800E27FF0C CRC64;
                                                                                      NAD(P)(+)--ARGININE ADP-
RIBOSYLTRANSPERASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas chlororaphis (Pseudomonas aureofaciens).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                           BY SIMILARITY.
                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonadaceae; Pseudomonas.
PRINTS; PR00970; RIBTRNSFRASE.
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InterPro; IPR003495; CobW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 HG----SDP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 EGLGHREGDP 307
                                                                      31
                                                                                                                          312
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SEQUENCE 419 AA; 4
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SEQUENCE
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TRAINING TISSEE-Cerebellum, and Spleen;

RA ATAINNOD'T TISSEE-Cerebellum, and Spleen;

RA MEDLINE=22354683; PubMed=12466851;

RA MEDLINE=22354683; PubMed=12466851;

RA MIRaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Klyosawa H.,

RA Nikaido I., Osato N., Baito R., Suzuki H., Yamanaka I., Klyosawa H.,

RA Baidarelli R., Hill D.P. Bult C., Hume D.A., Quackenbush J.,

RA Baike J.A. Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,

RA Blake J.A., Bradt D., Printic V., Chothia C., Corbani L.B., Cousins S.,

RA Garimond S., Gustinoido B., Hirokawa N., Jackson I.J., Jarvis B.D.,

RA Grimmond S., Gustinoido B., Hirokawa N., Jackson I.J., Jarvis B.D.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Maglott D.R., Maltais J.U., Don' D., Ramachandran S.,

Revasi T., Need J.C., Semple C.A., Setou M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Verardo R., Wagner L., Wahlestedt C., Marchion I., Matanabe Y., Weils C.,

Willming L.G., Wymshaw-Borris A., Yanaqisawa M., Yang I., Yang L.,

RA Miraki T., Waki K., Kawai J., Aiawa K., Arakwa T., Fukuda S.,

RA Miraki R., Yashikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Rhirak J., Waki K., Kawai J., Aiawa K., Arakwa T., Fukuda S.,

Ramishi A., Yoshino M., Waterston R., Banachi A., Sakazume N., Saro K.,

Ramishi A., Yoshino M., Waterston R., Bander B.S., Rogers J.,

Ramishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

Ramishi S., Hayashizaki Y.,

Ramishi S., Rawai S., Yang L.,

Ramishi S., Rawai S., Yang L.,

Ramishi S., Rawai S., Yang L.,

Ramishi R.,                                                                                    85 ALFSGSEGQLKPGARIFS-------FDGRDVLQHPAWPRKSVWHGSDPSGR 128
                                                                                                                                                                                                                      199 AVHAILAG-LNPSARIMPMAHGNVALSSLLDTHLFÖLPSLAASPGWMRK--MEATÖTPAS 255
                                                 26 IRGADFOCFOQARAAGLAGTFRAFLSSR-LODLYSIVRRADRTGVPVVNLRDEVLFPSWE 84
                                                                                                                                                                                                                                                                                 129 RLTDSYCET---WRTEAPAATGQASSLLA----GRLLEQEA---ASCRHAFVVLCIEN 176
                                                                                                                                                                                                                                                                                                                256 E-SDIYGVISWVYRERAPFHPQRLLEFLQKPWHNGRLLRSKGYFWLASRHLEIGLLAQS 313
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STRAIN=Crach II, and FVB/N; TISSUB-Breast cancer;
MEDLINE=2238257; PubMed=12477932;
Strausberg R.L., Fethgold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Butchow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshhyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
76; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Last annotation update)
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Nature 420:563-573(2002).
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270 S---FILRPHTALFTPDGLDELH------SDFDLSRVPDSCC-PWEPAHPLVL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           respiratory syndrome.";
Science 300:1394-1399(2003).
                                                      147 GQASSLLAGRLLE 159
                                                                                       314 -- LANLLSGRILK 324
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                                                                                                                                                                                   RIAB_CVHSA
                                                                                                                                                                RESULT
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Warzh D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz N.M., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
I.Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. US.A. 99:16899-16803(2002).
I. Proc. Natl. Acad. Sci. US.A. 99:16899-16903(2002).
Sactivity via RICK (CARDIAK, RIP2) and IKK-gamma. Confers
Responsiveness to intracellular bacterial lipopolysaccharides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 TYMD--TLMELVGFUNENLGSLGGLDCLLDHSTGVLNEHGETVFVFGDAGVGKSMLLQRL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 SGSEGQLK-PGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSYCETWRTEAPAAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 THODFOLVLHLVALNSFOPGGMRGI-----RGADFQCFQQARAAGLAGTFRAFLSSRL 54
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                                                                                                                                                                                                                                                                                                                                     (By similarity).
T: Self-associates. Binds to caspase-9 and RICK by CARD-CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Indels 61; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.9%; Score 76.5; DB 1; Length 953;
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                                                                                                                                                                                                                                                                                                                                                                             interaction (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Contains 1 CARD domain.
--- SIMILARITY: Contains 1 NACHT domain.
--- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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LRR 4.
LRR 5.
LRR 6.
LRR 6.
LRR 7.
LRR 9.
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InterPro; IPR001315; CARD.
InterPro; IPR007091; LRR RNinh.
InterPro; IPR007111; NACHT_NTPase.
Pfam; PP00619; CARD; 1.
Pfam; PP00519; NACHT; 1.
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JOMAIN 15 CAR
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EMBL, AK089662, BAC40940.1, -.
EMBL, BC042670, AA442670.1; -.
EMBL, BC043670, AA443670.1; -.
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Best Local Similarity 24.4%;
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PROSITE; PS50837; NACHT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47; Conservative
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702
702
702
755
765
8839
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8867
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NP BIND
REPEAT
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VARIANT
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TID RIAB CVHSA STANDARD, PRT, 7073 AA.

AC P59541; Q808C0; Q80BV7; Q80BV8; Q80E51;

DT 10-CCT-2003 (Rel. 42, Lest sequence update)

DT 10-CCT-2003 (Rel. 42, Last sequence update)

DT 10-CCT-2003 (Rel. 43, Last sequence update)

DE 15-WAR-2004 (Rel. 43, Last sequence update)

DE 16-WAR-2004 (Rel. 43, Last sequence upd
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MEDLINE=22660725; PubMed=12730501;

MEDLINE=22660725; PubMed=12730501;

MEDLINE=22660725; PubMed=12730501;

MEDLINE=22660725; PubMed=12730501;

Marra M.A., Once S.J., Asano J.K., Barber S.A., Chan S.Y.,

Cloutier A., Coughlin S.M., Freeman D., Girn N., Griffith O.L.,

A Leach S.K., Mayor M., McDonald H., Montgomery S.B., Pandoh P.K.,

A Perracad A.S., Robertson A.G., Schein J.E., Siddiqui A., Smallus D.E.,

Stott J.M., Yang G.S., Plummer F., Andonov A., Artsob H., Bastien N.,

A Berrard K., Booth T.F., Bowness D., Czub M., Drebot M., Pernando L.,

Flick R., Garbutt M., Gray M., Grolla A., Jones S., Feldmann H.,

Meyers A., Kabani A., Li Y., Mormand S., Stroher U., Tipples G.A.,

A Tyler S., Vogrig R., Ward D., Watson B., Brunham R.C., Krajden M.,

Petric M., Skownoski D.M., Upton C., Roper R.L.;

The genome sequence of the SARS-associated coronavirus.";
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STRAIN=Isolate Urbani,
MEDLINE=22660724; PubMed=12730500;
MEDLINE=22660724; PubMed=12730500;
MEDLINE=22660724; PubMed=12730500;
MICHOGUE D.A., Oberste M.S., Monroe S.S., Nix W.A., Campagnoli R.,
Icenogle J.P., Penaranda S., Bankamp B., Maher K., Chen M.-H.,
Tong S., Tamin A., Lowe L., Frace M., DeRisi J.L., Chen Q., Wang D.,
Erdman D.D., Peret T.C.T., Burns C., Kaiazek T.G., Rollin P.E.,
Sanchez A., Liffick S., Holloway B., Limor J., McCaustland K.,
Olsen-Rasmussen M., Fouchier R., Guenther S., Osterhaus A.D.M.E.,
"Characterization of a novel coronavirus associated with severe acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Isolate CUHK-SulO, and Isolate CUHK-W1;
MEDLINE=22737955; PubMed=12853594;
Tsul S.K.W., Chim S.S.C., Lo Y.M.D.;
"Coronavirus genomic-sequence variations and the epidemiology of the severe acute respiratory syndrome.";
New Engl. J. Med. 349:187-188(2003).
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MEDININE-Z2913660; PubMed=12958366;
Guan Y., Zheng B.J., H. Zhang Y.D., Liu X.L., Zhuang Z.X., Cheung C.L.,
IUO S.W., Lim P.H., Zhang L.J., Guan Y.J., Butt K.M., Wong K.L.,
Chan K.W., Lim W., Shortridge K.F., Yuen K.Y., Peiris J.S.M.,
Poon L.L.M.;
"Isolation and characterization of viruses related to the SARS
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STRAIN=ISOLATE HKU-39849;
MEDLINE=22758472; PubMed=12876307;
Zeng F.Y., Chan C.W., Chan M.N., Chen J.D., Chow K.Y.C., Hon C.C.C.,
Hui R.K.H., Li J., Li V.Y.Y., Wang C.Y., Wang P.Y., Guan Y., Zheng B.,
Poon L.L.M., Chan K.H., Yuen K.Y., Peiris J.S.M., Leung F.C.;
"The complete genome sequence of severe acute respiratory syndrome coronavirus strain HKU-38849 (HK-39).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruan Y., Wei C.L., Ling A.E., Vega V.B., Thoreau H., Se Thoe S.Y., Chia J.-M., Ng P., Chiu K.P., Lim L., Zhang T., Chan K.P., Oon L.B.L., Ng M.L., Leo S.Y., Ng L.F.P., Ren E.C., Stanton L.W., Long P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruan Y., Wei C.L., Ling A.E., Vega V.B., Thoreau H., Se Thoe S.Y., Chia J.-M., Ng P., Chiu K.P., Lim L., Zhang T., Chan K.P., Oon L.E.L., Ng M.L., Leo S.Y., Ng L.P.P., Ren E.C., Stanton L.W., Long P.M.,
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STRAIN=ISOlate BJ01, Isolate BJ02, Isolate BJ03, Isolate BJ04,
STRAIN=ISOlate BJ01, Isolate BJ02, Isolate BJ03, Isolate BJ04,
and Isolate GD01,
Qin E., Zhu Q., Yu M., Fan B., Chang G., Si B., Yang B., Peng W.,
Ji X., Lu F., Tang C., Yang R., Cao W.S., Wang J., Chen W., Cong L.,
Deng Y., Dong W., Han Y., Hu W., Lei M., Li C., Li G., Li G., Li H.,
Li S., Li W., Li W., Lin W., Liu J., Liu Z., Lu H., Ni P.,
Qi Q., Sun Y., Tang L., Tong Z., Wang J., Wang X., Wu Q., Xi Y.,
Zhou J., Yang L., Ye C., Ye J., Zhang B., Zhang F., Zhang J., Zhang X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Isolate TW1;
Yes S.-H., Kao C.-L., Tsai C.-Y., Liu C.-J., Chen D.-S., Chen P.-J.;
Whe complete genome of SARS coronavirus clone TW1.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
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Eickmann M., Becker S., Klenk H.-D., Doerr H.W., Stadler K.,

Censini S., Guidotti S., Masignani V., Scarselli M., Mora M.,

Donati C., Han J., Song H.C., Abrignani S., Covacci A., Rappuoli R.,

"SARS virus is a close relative of type II coronaviruses.";

Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
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Thiel V, Hertzig T., Putics A., Ivanov K.A., Schelle B., Bayer S.,
Scheiner B., Weinand H., Weissbrich B., Ziebuhr J.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
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Lancet 361:1779-1785(2003).
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STRAIN=Isolate Sin2500, Isolate Sin2677, Isolate Sin2679,
Isolate sin2774, and Isolate Sin2748;
MEDLINE=22667074; PubMed=12781537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taiwan.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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coronavirus from animals in southern China."; Science 302:276-278(2003).
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1613 HTLDESFLGRYMSALNHTKKWKFPQVGGLTSIKWADNNCYLSSVLLALQQLEVKFNAPAL 1672
 55 QDLYSIVRRADRTGVPVVNLRDEVLFPSWEALFSGSRGQLKPGARIFSFDGRDVLQHPAW 114
 1 HTHQDFQLV1HLVALNS-----PQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRL 54
 STRAIN=Isolate Taiwan TC1, Isolate Taiwan TC2, and Isolate Taiwan TC3;
Chang J.-G.C., Lin T.-H., Chen C.-M., Lin C.-S., Chan W.-L.,
 STRAIN=Isolate Taiwan;
Lin J.-H., Chiu S.-C., Yang J.-Y., Wang S.-F., Chen H.-Y.;
"Detection of a novel human coronavirus in a severe acute respiratory
 7.9%; Score 76; DB 1; Length 7073;
22.1%; Pred. No. 2e+02;
ative 24; Mismatches 73; Indels 30; Gaps
 CHARACTERIZATION OF HELICASE.
MEDLINE=22890296; PubMed=12917423;
Tanner J.A., Watt R.M., Chai Y.-B., Lu L.-Y., Lin M.C., Peiris J.S.
Poon L.L.M., Kung H.-F., Huang J.-D.;
"The severe acute respiratory syndrome (SARS) coronavirus
"The severe belongs to a distinct class of 5' to 3' viral
 MEDLINE=22690353; PubMed=12746549;
Anand K., Ziebuhr J., Wadhwani P., Mesters J.R., Hilgenfeld R.;
 STRAIN=Isolate Shanghai LY;
Yuan Z., Zhang X., Hu Y., Lan S., Wang H., Zhou Z., Wen Y.;
Stumitred (JTD-2003) to the EMBL/GenBank/DDBJ databases.
 STRAIN=Isolate Shanghai QXC;
Yuan Z., Zhang X., Hu Y., Lan S., Wang H., Zhou Z., Wen Y.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
 SEGUENCE FROM N.A.
STRAIN=Isolate_TWH, Isolate TWJ, Isolate TWK, Isolate TWS.
 3D-STRUCTURE MODELING OF 3241-3540, AND CHARACTERIZATION.
 Snin M.-C.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 SEQUENCE FROM N.A.
STRAIN=Isolate HSR 1;
Canducci F., Clementi M., Poli G., Vicenzi E.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 STRAIN=Isolate AS;
Balotta C., Corvasce S., Violin M., Galli M., Moroni M.,
Vigevani G.M., Ruan Y.J., Salemi M.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
 STRAIN=Isolate Vietnam;
Emery S., Erdman D.D., Peret T.C.T., Ksiazek T.G.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
 syndrome patient in Taiwan.";
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 and Isolate TWY;
Shu H.Y., Wu K.W., Tsai S.F.; BL/GenBank/DDBJ databases.
Showntted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 Wang Z., Cheng S., Zhang Y.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
 SEQUENCE OF 1-507; 1655-5170 AND 6903-7073 FROM N.A.
 SEQUENCE OF 497-1674 AND 5158-6911 FROM N.A.
 J. Biol. Chem. 278:39578-39582(2003).
 SEQUENCE OF 4993-5127 FROM N.A.
 SEQUENCE OF 4993-5136 FROM N.A.
 SEQUENCE OF 1-322 FROM N.A.
 Query Match
Best Local Similarity 22.1*
---hes 36; Conservative
 STRAIN=Isolate ZJ-HZ01;
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1673 QEAYYRARAGDANFCALIL-----AYSNKTVGELG------DVRETWIH--- 1711
 MEDLINE=9734980; PubMed=9205837;
MEDLINE=97349980; PubMed=9205837;
Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Yamamoto Y., Aiba H., Baba T., Hayashi K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uchara K., Wada C.,
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"Construction of a contiguous 874-kb sequence of the Escherichia coli
- KI2 genome corresponding to 50.0-68.8 min on the linkage map and
DNA Res. 4:91-113(1997).
 SEQUENCE FROM N.A.
STRAIN=06.HJ / CFT073 / ATCC 700928;
STRAIN=06.HJ / CFT073 / BLC 700928;
WEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Rosech P.,
Rasko D., Bucklee B.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose B.L., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
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of uropathogenic Escherichia coli.";
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Aha exopolyphosphatase of Escherichia coli. The enzyme and its ppx
gene in a polyphosphate operon.";
J. Biol. Chem. 268:633-639(1993).
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SEQUENCE FROM N.A.
STRAIN-RIZ / MGJ6559
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
 Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
 PPX ECOLI STANDARD; PRT; 512 AA.
PS904.; P7681, 24,
01-DE-1992 (Rel. 24, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Excopolyphosphatase (EC 3 6.1.11) (Excopolyphosphatase)
PPX OR B2502 OR C3020 OR Z3765 OR ECS3364.
Escherichia coll, 6, and
Escherichia coll 0157:H7.
 STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Maybew G.F., Evans P.S., Gregor J., Kirkparrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997)
 1712 ---LLQHANLESAKRVLNVVCKHCGQKTTTLTGVEAVMYMGTL 1751
 115 PRKSVWHGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRL 157
 [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
 MEDLINE=93107072; PubMed=8380170
 MCBI_TaxID=562, 217992, 83334;
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RX MEDLINE=94025037; PubMed=8212131;
RX Relzer J., Relzer A., Saler M.H. Jr., Bork B., Sander C.;
RX Relzer J., Relzer A., Saler M.H. Jr., Bork B., Sander C.;
RY Phosphates belong to the sugar kinase/actin/hsp 70 superfamily.";
RY Phosphates belong to the sugar kinase/actin/hsp 70 superfamily.";
RY Trends Bicchem. Sci. 18:247-248 (1993).
CC -: FUNCTION: DEGRADATION OF INORGANIC POLYPHOSPHATES. ORTHOPHOSPHATE
CC IS RELEASED PROCRESSIVELY FROM THE ENDS OF POLYPHOSPHATE POORLY
CC STORESIDUES LONG, BUT CHAINS OF CIRCA 15 RESIDUES COMPETE POORLY
CC -: CATALYTIC ACTIVITY: RPOLYPHOSPHATE.
CC (POLYPHOSPHATE & SUBSTRATE.
CC (POLYPHOSPHATE & CORPACION: Membrane-associated.
CC -: SUBGILILLULAR LOCATION: Membrane-associated.
CC -: SUBGILLULAR LOCATION: Membrane-associated.
CC -: SUBCILLULAR LOCATION: Membrane-associated. 90 SEGQLKPGARIFSFDGR----DVLQHPAWPRKSVWHGSDPSGRRLTDS---YCETWRTEA 142 SEQUENCE FROM N.A.
STRATS-1219-17 / RIND 0509952;
STRATS-1219-115-6231;
BADDINE-2115-6231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohlesubo E., Nakayama K., Murata T., Tanada M., Tobe T.,
Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
"Ols7:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001). 20 PGGMRGIRGADFOCFOQAR-------AAGLAGIFRA-----49 ----FLSSRLQDLY-SIVRRADRIGVPVVNLRDE--VLFPSWEALFSG------69; Gaps Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001). DB 1; Length 512; 79; Indels 512 AA; 58004 MW; 48611AFF5D9FB9C3 CRC64; R EMBL; D90880; BAA16390.1; -R EMBL; D90880; BAA16390.1; -R EMBL; AE016764; AAR81470.1; -R EMBL; AE005479; AA67512.1; -R EMBL; AE0056479; AA67512.1; -R EMBL; AE0056479; AA6787.1; -R PIR; D91049; Ouery Match
7.8%; Score 75.5; DB
Best Local Similarity 21.1%; Pred. No. 11;
Matches 48; Conservative 32; Mismatches EMBL; 106129; AAA24415.1; -. EMBL; AE000336; AAC75555.1; -. <del>-</del> SEQUENCE

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292 SDGALREGV-LYEMEGRFRHQDVRSRTASSLANQYHIDSEQARRVLDTTMQMYEQWREQQ 350
 TISSUELLYMPHO.

WE MIDLINE-22386257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Colline F.G., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
A Batchenko L., Marushia K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J. Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Mullahy S.J.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Hilalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hilling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E.,
A Generchion and, initial analysis of more than 15,000 full-length
Human and mouse conna Sci. U.S.A., 99:16899-16903(2002).
 MEDLINE=22682943; PubMed=12798037; Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.; Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.; Comput. Biol. Chem. 27:29-34 acterizing protein forms."; -1- CAPALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
 143 P-AATGOASSLLAGRLLEQEAA----SCRHAFVVLCIENSVMTSFSK 184
 351 PKLAHPQLEALLRWAAMLHEVGLNINHSGLHRHSAYILQNSDLPGFNQ 398
 IS-MAR-2004 (Rel. 43, Created)
IS-MAR-2004 (Rel. 43, Last sequence update)
IS-MAR-2004 (Rel. 43, Last annotation update)
Serine/threonine-protein kinase pim-3 (EC 2.7.1.37).
 PRT; 326 AA
 EMBL, BC052239; AAH52239 1; ALT INIT.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Fram, PF00009; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
SWART; SW00220; S TKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 STANDARD;
 IDENTIFICATION FROM ESTS.
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
 subfamily.
 PIM3 HUMAN
 RESULT 13

PIN3 HUMAN

PLO PIN3 HUMAN

AC Q86V86,

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120 LLVLERPEP-----AQDLFDFITERGALDEPLARRFFAQVL----AAVRHCHSCGVVH 168
 72 VNLRDEVLFPSWEA----LFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDFS- 126
 169 RDIKDENÍLVDLRSGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATV 226
 12 LVALNSPOPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRIGVPV 71
 ; Score 73.5; DB 1; Length 326; ; Pred. No. 9.9; 12; Mismatches 82; Indels 25; Gaps
 Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakanino K., Masuda S., Miki T., Mizobuchi K., Sampei G., Seki Y., Tagami H., Takemoto K., Mada C., Yamamoto Y., Saito N., Yano M., Horiuchi T., "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
 STRAIN=KI2 / MG1655,
MBDLINB=7426617, PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein ycds precursor.
Hypothetical protein ycds precursor.
YCDS OR B1024 OR 21256 OR ECS1270.
Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae, Escherichia.
 STRAINS-OIST. T. SDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
MEDLINE-21074935; PubMed=11206551;
Rose D.J., Maybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dinalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
PROSITE; PS00108; PROTEIN KINASE ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
Phosphorylation.
 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
 41FDF9DD2467A162 CRC64;
 127 ---GRRLIDSYCETWRIBAPATGQASSLLAGRLLEQEAAS 164
 229 WSLGVLLYDMVCGDIPFE-----ODEFILRGRLLFRRRVS 263
 ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
 BY SIMILARITY
 MEDLINE=97061202; PubMed=8905232;
 40 293 PRK
46 54 ATI
69 ATI
170 170 BY
326 AA; 35863 MW;
 01-NOV-1997 (Rel. 35, Created)
 7.68;
 Query Match 7.6%;
Best Local Similarity 26.1%;
 42; Conservative
 STANDARD;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Mau B., Shao Y.;
 YCDS ECOLI
P75907;
 STRAIN=K12;
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RA HARASHI T., Makino K., Ohnsibil M., Kurokawa K., Tanaka M., Tobe T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

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RA Han C.-G., Ohtsubo E., Nakayama K., Murata T.,

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RA Han C.-G., Ohtsubo E., Nakayama K., Murata T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T.,

RA Han C.-G., Ohtsubo E., Nakayama M., Tobe T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T.,

RA Han C.-G., Ohtsubo E., Ohtsubo E., Nakayama M., Tobe T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T.,

RA Han C.-G., Ohtsubo E., Nakay
 58 YSIVRRADRIGVPVVNLRDEVLFP----SWE--ALFSGSEGQLKPGARIFSFDGRDVLQH 111
 528 --IDAEGPDSGKHDVDLTTIVYSPPLKDNWRGFÄGFGYADGÖFSEGKGIV----RDWLAG 581
 2 THODEO---LULHLVALNSPO-PGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLODL 57
 NA95 HUMAN STANDARD; PRT; 646 AA.
Q9UGMG; Q9UGMG;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Neighbor of Akinase anchoring protein 95 (Homologous to AKAP95
Neighbor of Akinase A-binding protein 95) (HAP95) (HRIHFB2018).
NARAP95.
 43; Gaps
 sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 EMBL, AE000204; AAC74109.1; -
EMBL, D90739; BAA35806.1; -
EMBL, D90740; BAA35809.1; -
EMBL, D90740; BAA35809.1; -
EMBL, AE005302; AAG5642.1; -
EMBL, AF0002554; BAB34693.1; -
PIR; F64844; F64844.
PIR; F64844; F64846.
Interpro; IPR008940; Prenyl_trans.
Interpro; IPR001440; TPR.
Hyporhetical protein; Outer membrane; Signal; Complete proteome.
SIGNAL
 7.6%; Score 73.5; DB 1; Length 807; 26.1%; Pred. No. 28;
 Query Match
Best Local Similarity 26.1%; Pred. No. 28;
Marches 42; Conservative 16; Mismatches 60; Indels
 POTENTIAL. HYPOTHETICAL PROTEIN YCDS.
 SEQUENCE 807 AA; 92207 MW; B20067C3D41723FD CRC64;
 112 PAWPRKSVW------HGSDPSGRRLTDSY--CETWR 139
 582 VEWRSRNIWLEAEYAERVFNHEHKP-GARLSGWYDFNDNWR 621
 Nature 409:529-533(2001)
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
TISSUE=Fetal brain;
 HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
 Sequence From Ann.

TISSUBE-Placenta,

MEDLINE-2238857; Pubmed=12477932;

MEDLINE-2238857; Pubmed=12477932;

REDLINE-2388657; Pubmed=12477932;

REDLINE-2388657; Pubmed=12477932;

REDLINE-2388657; Pubmed F.S., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Babat N.R.,

A Altschul S.F., Jacdan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusham K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusham R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., McWarn P.J., McKernan K.J., Malek J.J., Hulyk S.W.,

Richards S., Morley K.C., Halte S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

Nillalon D.K., Mandan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Shalska U., Smailus D.E.,

Generation and mouse CDNa sequences ", Schore than 15,000 full-length

Human and mouse CDNA sequences ", Formur S. Monta M.A.;

Florc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 MEDLINE=20163068; PubMed=10697960; Seti N., Unramatsu M.-A.; Seti N., Ueki N., Yano K., Saito T., Masuho Y., Muramatsu M.-A.; sch N., Toki N., Ineighbor of A-kinase anchoring protein 95 (AARP95) on chromosome 19p13.11-p13.12 region."; J. Hum. Genet. 45:31-37(2000).
 TISSUE=Placenta, and T-cell lymphoma;
MEDLINE=20347256; PubMed=10748171;
Mestberg C., Yang J.-P., Tang H., Reddy T.R., Wong-Staal F.;
Wa novel Buttle protein binds to RNA helicase A and activates the retroviral constitutive transport element.";
 SEQUENCE FROM N.A.
MEDILIPE-2022233; PubMed=10761695;
Orstavik S., Eide T., Collas P., Han I.O., Tasken K., Kieff E., Jahnsen T., Skalhegg B.S.;
Jahnsen T., Skalhegg B.S.;
Tidentification, cloning and characterization of a novel nuclear protein, HA95, homologus to A-kinase anchoring protein 95.";
Biol. Cell 92:27-37(2000).
 EMBL; A3025905; BAA85003.1; -.
EMBL; AJ243467; CAB65092.1; -.
EMBL; ART99414; AAR8648.1; -.
EMBL; BC000713; AAH00713.1; -.
EMBL; AB015332; BAA34791.1; ALT_INIT.
GO; GO:0005634; C:nucleus; TAS.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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Ouery Match 7.5%; Score 72.5; DB 1; Length 646;
Best Local Similarity 26.2%; Pred. No. 27;
Matches 39; Conservative 11; Mismatches 68; Indels 31; Gaps 8;
 96 NORLDMVPHLE--TDMMQGGVYGSGGERYDSYESCDS------RAVLSER--DLY---- 140
 63 RADRIGVPVVNLRDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVWHG 122
 141 ---RSGYDYSELD----PEMEMAY---BGGYDAYRDQFRMRGNDTF----GPRAQGWAR 185
 3 HODFOLVLHLVALNSPOPGGMRGIRGADFOCFQQARAAGLAGTFRAFLSSRLODLYSIVR 62
GO, GO:0017151; F:DEAD/H-box RNA helicase binding; TAS. InterPro; IPR007071; AKAR995.
Efam: PF04998; AKAP95; 1.
SMART; SM0335; ZAF C2H3; 1.
DOMAIN 274 213; 217 2187; 2187
 123 SDPSGRRLTDSYCETWRTEAPAATGQASS 151
 186 DARSGRPMASGYGRMWE-DPMGARGQCMS 213
 646 AA; 71640 MW;
 640
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 1 HTHQDFQLVLHLVALNSPQP.........CRHAFVVLCIENSVMTSPSK 184
 Description
 1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1017041 segs, 315518202 residues
 SUMMARIES
 OM protein - protein search, using sw model
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Q61434
Q9QZD2
 093419
09CRT2
 sp arches: *
sp bacteria: *
sp bacteria: *
sp lungi: *
sp invertebrate: *
sp mammal: *
sp mammal: *
sp phage: *
sp phage: *
sp phage: *
sp plage: *
sp plage: *
sp vertebrate: *
 Q9WUWS
 Q8NG19
Q8N4S4
 QBAWC6
 Q86SC8
Q96T70
 Gapop 10.0 , Gapext 0.5
 sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-938-391-4
966
 Query
Match Length DB
 SPIREMBL 25:*
 BLOSUM62
 88677777888844
648787148788477
6446784406447
 Perfect score:
 Scoring table:
 Score
 Database :
 Sequence:
 Searched:
 Run on:
 Title:
 Result
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5 HSHRDEQPVLHLVALNSPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSI 64 1 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI

60

0; Gaps

Query Match 86.4%; Score 835; DB 4; Length 187; Best Local Similarity 85.1%; Pred. No. 5.1e-76; Matches 154; Conservative 14; Mismatches 13; Indels

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| QBmse3 drosophila QBmt89 drosophila QB6bhi drosophila O1786 caenorhabdi Q9u9k7 caenorhabdi Q8u9k7 caenorhabdi Q8u9k7 caenorhabdi Q8u9k9k1 kradyrhiroh | יים בע בב אייי                                                                                                                                                                                                   | Q8xeeO escherichia                                                                                                   | ta, Buteleostomi, dae, Homo. in expressed in Pichia CRC64;                                                                                                                                                                                                                                                                                                |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Q8MSE3<br>Q8MT89<br>Q86BH1<br>Q9U9K6<br>Q9U9K7<br>Q9U9K7<br>Q8U0G6                                                                                    | 992K28<br>052660<br>052679<br>0972A9<br>087472<br>087673<br>0916710<br>098764<br>098764<br>098764<br>098764<br>098771<br>086W(3)<br>098172<br>098172<br>098172<br>098172<br>098172<br>098172<br>098172<br>098172 | Q8XEED ALIGNMENTS ALIGNMENTS PRT; 187 AA. Created) Last sequence update) Last sequence update)                       | iata; Vertebra<br>rrhini; Homini<br>J.;<br>ified endostat<br>-282(2001).                                                                                                                                                                                                                                                                                  |
|                                                                                                                                                       | 200000000000000000000000000000000000000                                                                                                                                                                          | 900                                                                                                                  | ites;<br>1151<br>X., X.,<br>ro o<br>ao 1<br>1; -                                                                                                                                                                                                                                                                                                          |
| <b>்</b> வ்சுவ்வைவ் வ                                                                                                                                 | 9.8<br>9.7<br>7.702<br>9.0<br>9.0<br>9.0<br>9.0<br>9.0<br>9.1<br>2.8<br>8.7<br>2.8<br>8.5<br>8.5<br>8.5<br>8.5<br>8.5<br>8.5<br>8.5<br>8.5<br>8.5<br>8                                                           | LIMINARY;  EMBLES: EMBLES: EMBLES: EMBLES: EMBLES: (Fragment)                                                        | Deficiency September (Jumman).  Enkaryota, Metazoa, Chordata, Cran Mammalia; Eutheria, Primates, Cata NCBL_TaxID=9666;  [1]  SEQUENCE FROM N.A.  MEDLINE=11409409, PubMed=11517600, FERGY Y., Cui L.B., Liu C.X., Ma Q. "Inhibition effect in vitro of pur Shorn Wu Gong Cheng Xue Bao 17:278 BMBL, AR416592, AAL37720.1;  SEQUENCE 187 AA, 20448 MW, 72B |
|                                                                                                                                                       | 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                          | LT 1  SGHXXIS,  OH-MAR-2002 (Tr  OL-MAR-2002 (Tr  OL-MAR-2002 (Tr  CL-MAR-2002 (Tr  CL-MAR-2002 (Tr  CL-MAR-2002 (Tr | Endone sapisates (Human)  Bukaryota, Mammalia; Butheria;  MCBI_TaxID=9606;  [1]  SEQUENCE FROM N.A.  MEDLINE=2140940; P.  MEDLINE=2140940; P.  "Inhibition effect Sheng Wu Gong Cheng Sheng Wu Gong Cheng Sheng Wu Gong TeR  NON TER  SEQUENCE 187 AA,                                                                                                    |
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 79 HSHRDFQPVLHLVALNSPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSI 138
 61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120
 121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVWT 180
 199 HGSDPNGRRLTESYCETWRTEAPSATGQASSLLGGSALGGSAASCHHAYIVLCIENSFMT 258
 1 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI 60
 0; Gaps
 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last sequence update)
Multi-functional protein MFP.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Ouery Match 86.4%; Score 835; DB 4; Length 261; Best Local Similarity 85.1%; Pred. No. 7.8e-76; Matches 154; Conservative 14; Mismatches 13; Indels
 86.4%; Score 835; DB 4; Length 816; 85.1%; Pred. No. 3.3e-75;
 Straugherg R.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC039715, AAH33715.1; InterPro; IPR008161; Clg helix. InterPro; IPR008161; Collagen.
 Dou D.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF282883; AAMS2249.1; -.
SEQUENCE 261 AA; 26745 MW; CA60C920AF3E90E5 CRC64;
 816 AA; 82553 MW; 5D539B2946694F86 CRC64;
 01-0CT-2002 (TrEMBLrel, 22, Created)
01-0CT-2002 (TrEMBLrel, 22, Last sequence update)
01-UUN-2003 (TrEMBLrel, 24, Last annotation update)
Similar to collagen, type XVIII, alpha 1 (Fragment).
 261 AA.
 PRT; 816 AA.
 PRT;
 Pfam; PF01391; Collagen; 5.
ProDom; PD000007; Clg_helix; 1.
 FISSUE=Renal adenocarcinoma;
 PRELIMINARY;
 PRELIMINARY;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 181 S 181
 185 A 185
 181 S 181
 259 A 259
 NON TER
SEQUENCE
 Collagen.
 Q8N4S4
Q8N4S4;
 QBNG19
 RESULT 2
08NG19
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 957 HTHODPOPVLHLVALNTPLSGGMRGIRGADPOCFOQARAVGLSGTFRAFLSSRLODLYSI 1016
 1017 VRRADRGSVPIVNLKDEVLSPSWDSLFSGSGQGLQPGARIFSFDGRDVLRHPAWPQKSVW 1076
 61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120
 121 HGSDPSGRRITDSYCETWRTBAPAATGQASSLLAGRILLEQBAASCRHAFVVLCIENSVMT 180
 634 HSHRDPQPVLHLVALNSPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSI 693
 754 HGSDPNGRRLTESYCETWRTEAPSATGQASSLLGGGRLLGGSAASCHHAYIVLCIENSFWT 813
 61 VRRADRICVPVVNLRDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLOHPAWPRKSVW 120
 121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEGEAASCRHAFVVLCIENSVMT 180
 9
 1 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLQDLYSI
 0; Gaps
 1 HTHODPOLVLHLVALNSPOPGGMRGIRGADPOCPOQARAAGLAGTFRAFLSSRLQDLYSI
 0; Gaps
 Abe N., Muragaki Y., Yoshioka H., Inoue H., Ninomiya Y.;
"Identification of a novel collagen chain represented by extensive interruptions in the triple-helical region.";
Cell. Mol. Biol. Res. 196:576-582(1993).
EMBL; D27546; BAA04483.1; -...
PIR; B56101; B56101.
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
NCBL_TaxID=10090;
 86.0%; Score 831; DB 11; Length 1140;
83.7%; Pred. No. 1.3e-74;
tive 17; Mismatches 13; Indels 0;
Matches 154; Conservative 14; Mismatches 13; Indels
 SEQUENCE 1140 AA; 115156 MW; 8B0C7E6862B3BDFE CRC64;
 MGD; MGI:88449; COlISal.

GO; GO:0005199; F:structural molecule activity; IEA.

GO; GO:0007155; P:cell adhesion; IEA.

InterPro; IPR008161; Clq helix.

InterPro; IPR008160; ColIagen.

InterPro; IPR003129; TSPN.

Pfam; PF01391; Collagen; 8.

Pfam; PF0210; TSPN; 1.
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 PRT; 1140 AA
 ProDom, PD000007; Clg_helix; 1.
 Matches 154; Conservative
 PRELIMINARY;
 Collagen (Fragment).
 Mus musculus (Mouse)
 1137 SFSK 1140
 SEQUENCE FROM N.A.
 Best Local Similarity
 HSSP; P39061; 1KOE
 181 SFSK 184
 181 S 181
 814 A 814
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 43 HTHQDFHPVLHLVALNTPLSGGMRGIRGADFQCFQQARAVGLSGTFRAFLSSRLQDLYSI 102
 61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120
 121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180
 163 HGSDPSGRRLMESYCETWRTEATGVTGQASSLLSGRLLEQKAESCHNSYIVLCIENSFWT 222
 9
 TISSUB-Liver;
Jia J.D., Bauer M., Sedlaczek N., Ruehl M., Riecken B.O., Schuppan D.;
"Temporospatial expression of collagen XVIII/endostatin in acute and
 TISSUE=Liver;
Jia V.D., Bauer M., Eberspaecher U., Donner P., Schuppan D.;
Partial 3'-terminal cDNA sequence of rat collagen XVIII/endostatin.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 1 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFQQARAAGLAGTFRAFLSSRLQDLYSI
 Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
 Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 Gaps
 STRAIN=Sprague-Dawley,
MEDLINE=20227226; PubMed=10766159;
MEDLINE=20227226; PubMed=10766159;
Perlett G., Concari P., Giardini R., Marras E., Piccinini F.,
Folkman J., Chen L.;
"Antitumor activity of endostatin against carcinogen-induced rat
primary mammary tumors.";
Cancer Res. 60.1793-1796(2000).
EMBL, ARIB9709; AAF00975.1; -.
HNSPP, P39061; IKOE.
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 Match 84.2%; Score 813; DB 11; Length 226; Local Similarity 82.1%; Pred. No. 1.1e-73; es 151; Conservative 16; Mismatches 17; Indels (
 226 AA; 25350 MW; 38B83C0486C0E949 CRC64;
 0902D2;
0902D2;
01-MXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Collagen XVIII (Fragment).
 01-NOV-1999 (TrEMBirel. 12, Created)
01-NOV-1999 (TrEMBirel. 12, Last sequence update)
01-DEC-2001 (TrEMBirel. 19, Last annotation update)
Collagen type XVIII, alpha (I) chain (Fragment).
 PRT; 171 AA.
 PRT;
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 181 SFSK 184
 223 SFSK 226
 NCBI_TaxID=10116;
 SEQUENCE
 Query Match
 090ZD2
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 1161 HVHQDFQFALHLVALNIFLSGGMRGIRGADFQCFQQARQVGLAGTFRAFLSSRLQDLXSI 1220
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 69 VPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGR 128
 61 VPIVNLKDEVLSPSWDTLFSGSQGQLHSGARIFSFDGRDVLRHPAWPQKSVWHGSDFSGR 120
 9 VLHLVALNSPQPGGNRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTG 68
 9
 MEDLINE=98411346; PubMed=9738008; Halfter W., Dong S., Schurer B., Cole G.J.; Dong S., Schurer B., Cole XVIII is a basemant membrane heparan sulfate proteoglycan."; J. Biol. Chem. 273:25404-25412(1998).
 Collagen XVIII precursor.
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
 1 HTHODFOLVLHLVALNSPOPGGMRGIRGADFOCFOOARAAGLAGTFRAFLSSRLODLYSI
 0; Gaps
 0; Gaps
 129 RLIDSYCETWRTEAPARGQASSLLAGRLLEQEAASCRHAFVVLCIENSVM 179
 121 RLMESYCETWRTEATGVIGQASSLLSGRLLEQKAESCHNSYIVLCIENSFM 171
 Query Match
77.6%; Score 750; DB 13; Length 1344;
Best Local Similarity 76.1%; Pred. No. 2.3e-66;
Matches 140; Conservative 16; Mismatches 28; Indels 0;
 78.1%; Score 754; DB 11; Length 171; 81.9%; Pred. No. 6.5e-68; tive 16; Mismatches 15; Indels C
chronic liver injuries.";
Submitted (FES-1999) to the EMBL/GenBank/DDBJ databases.
EMBL AJ7366973; CR844263.1; -.
HSSP; P39061; IKOE.
 Halfter W., Dong S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF083461, AAC33294.2; -. 1939061; IXOE. GO; GO:00061199; F:structural molecule activity; IEA. GO; GO:0007155; P:cell adhesion; IEA.
 SEQUENCE 1344 AA; 137402 MW; 7AA366E4FE940CCD CRC64;
 NON TER 171 171 NON TER 171 AA; 18933 NW; 81BE2EE3FC2C8B72 CRC64;
 01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 PRT; 1344 AA
 POTENTIAL.
 Interpro; IPR008161; Clg helix.
Interpro; IPR008160; Collagen.
Interpro; IPR008965; Cond like_lec_gl.
Interpro; IPR001791; Laminin_G.
Interpro; IPR0011291; TSPN.
Pfam; PP01391; COllagen; 8.
Pfam; PP02210; TSPN, 1.
 01-NOV-1998 (TrEMBLrel. 08, Created)
 ProDom; PD000007; Cighelix; 2. SMART; SM00282; LamG; 1. SMART; SMO0210; TSPN; 1.
 Matches 140; Conservative
 PRELIMINARY;
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Collagen; Signal.
 NCBI_TaxID=9031;
 Query Match
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121 ATGQASSLLSGRLLEQKAASCHNSYIVLCIENSFMTSFSK 160

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STRAIN-CSTBL/6J; TISSUB-Embryo;

STRAIN-CSTBL/6J; TISSUB-Embryo;

X MEDLINE-2108566), PubMed=1121651;

X MEDLINE-2108566), PubMed=1121651;

X MEDLINE-2108566), PubMed=1121651;

X MEDLINE-2108566), PubMed=1121651;

X Mexan T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Matsuda H.A., Ashburner M., Badlov S., Casavant T.,

RA Aizawa K., Matsuda H.A., Ashburner M., Badlov S., Casavant T.,

RA Fleischmann W., Ashburner M., Badlarellov S., Casavant T.,

RA Fleischmann W., Stauli F., Tomita M., Wagner I., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baddarelli R., Barsh G.,

RA Sakai K., Okido T., Fletcher C., Fullita M., Wagner I., Washio T.,

RA Sakai K., Mill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Dronselm M.J., Bult C., Fletcher C., Fullita M., Monbaerts P.,

RA Dronselm M., Saco K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Byashizaki Y.,

RA Hayashizaki Y.,

RA Fluctional annosation of a full-length mouse cDNA collection.",

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***Theory of the collection of a full-length mouse cDNA collection.";
 1281 HGSDAKGRRLPESYCEAWRTDERGTSGQASSLSSGKLLEQSASSCQHAFVVLCIENSFWT 1340
61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVW 120
 121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180
 85 ALFSGSEGOLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGRRLTDSYCETWRTEAPA 144
 61 SIFSGSOGOLOPGARIFSFDGRDVLRHPAWPQKSVWHGSDPSGRRLMESYCETWRTETTG 120
 25 GIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTGVPVVNLRDEVLFPSWE 84
 1 GIRGADFQCFQQARAVGLSGTFRAFLSSRLQDLYSIVRRADRGSVPIVNLKDEVLSPSWD 60
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
 ó
 75.2%; Score 726; DB 11; Length 160; 83.8%; Pred. No. 4e-65; ive 16; Mismatches 10; Indels 0
 SEQUENCE 160 AA; 17725 MW; 60F853D777C375D2 CRC64;
 145 ATGQASELLAGRILEQEAASCRHAFVVLCIENSVMTSFSK 184
 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Procollagen, type XVIII, alpha 1 (Fragment).
 PRT; 160 AA.
 MGD; MGI:88451; Coll8al.
00; GO:0005604; C:basement membrane; IDA.
GO: GO:0001525; P:angiogenesis; IMP.
NON_TER
 01-JUN-2001 (TrEMBLrel. 17, Created)
 EMBL; AK014292; BAB29249.1; -. HSSP; P39061; 1KOE.
 Conservative
 PRELIMINARY;
 Nature 409:685-690(2001)
 Mus musculus (Mouse)
 1341 AAKK 1344
 Similarity
 181 SFSK 184
 134;
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1252 HGSDAKGRRLTESYCETWRTDESAVTSQASSLTSGKLLEQRPQSCNKNFIVLCIENSFMT 1311
 61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120
 121 HGSDPSGRRLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMT 180
 SEQUENCE FROM N.A.

Ishino T., Sekimizu K., Natori S., Kubo T.;

Ishino T., Sekimizu K., Natori S., Kubo T.;

Idenication and characterization of genes expressed selectively in the regenerating tail of Xenopus laevis tadpole.";

Submitted (Apd-2000) to the EMBL/GenBank/DDBJ databases.

BMBL, AB047066; BAB84674.1;

GO, GO:0007195; P:structural molecule activity; IEA.

GO; GO:0007155; P:sell adhesion; IEA.

InterPro; IPR008167; Clg helix.

InterPro; IPR008167; Clg helix.

InterPro; IPR003129; TSPN.

Pfam; PF01391; Collagen.

Pfam; PF01391; Collagen.

Pfam; PF01201; TSPN; 1.
 1 HTHQDFQLVLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI
 0; Gaps
 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Type XVIII collagen short variant
Xenopus laevis (African clawed frog)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 Type XVIII collagen alphal chain.
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 71.8%; Score 694; DB 13; Length 1315; 70.1%; Pred. No. 9.6e-61; ive 18; Mismatches 37; Indels 0;
 Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
 1315 AA; 134946 MW; 0C56C235DE058365 CRC64;
 SEQUENCE FROM N.A.
MEDLINE=22166979; PubMed≈12175494;
Elamaa H., Peterson J., Pihlajaniemi T., Destree O.;
 01-UTN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 PRT; 1307 AA.
 01-OCT-2002 (TrEMBLrel. 22, Created)
 clg_helix; 1.
 Local Similarity 70.1
 PRELIMINARY;
 PRELIMINARY;
 ProDom; PD000007; Clg_he.
SMART; SM00210; TSPN; 1.
 Xenopodinae, Xenopus.
NCBI_TaxID=8355;
 Xenopodinae; Xenopus.
NCBI_TaxID=8355;
 1312 NNRK 1315
 181 SFSK 184
 Collagen.
SEQUENCE
 Query Match
 Q8QHL9
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Q8QHL9
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69 VPVVNLRDEVLFPSWEALFSGSEGQLKFCARIFSFDGRDVLQHPAWPRKSVWHGSDPSGR 128
298 HGSDGRGHRQTDNYCETWRAGDRAVTGLASSLQAGQLLQQTSSSCSSSYIALCIENSYMT 357
 Hagg F.W., Horeall-Aultouien N., Saring D., Farolle I., Philaianien T.;

Pihlaianien T.;

"Cloning of mouse type XV collagen sequences and mapping of the corresponding gene to 481-3. Comparison of mouse and human alpha 1;

"Cloning of mouse type XV collagen sequences and human alpha 1;

"Collagenous domains.";

"Collagenous domains.";

"Collagenous domains.";

"EMBL, AF011450; AAC5387.1; -.

"REMBL, COLOSTISS, Picell adhesion; IEA.

"CO; GO:0007155; Picell adhesion; IEA.

"CO; GO:0007155; Picell adhesion; IEA.

"TherPro; IPR008161; Collagel."

"InterPro; IPR008195; ConA_like_lec_gl.

"InterPro; IPR001199; TSPN.

"Propon; PF02109; T
 1196 VIHLVALNIPVAGDIR----ADFQCFQQARAAGLLSTFRAFLSSHLQDLSTVVRXABRFG
 9 VLHLVALNSPQPGGMRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSIVRRADRTG
 129 RLTDSYCETWRTEAPAATGQASSLLAGRLLEQEAASCRHAFVVLCIENSVMTSFSK 184
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 4;
 Query Match 57.0%; Score 551; DB 11; Length 1367; Best Local Similarity 59.7%; Pred. No. 2.5e-46; Matches 105; Conservative 25; Mismatches 42; Indels 4;
 1367 AA; 140525 MW; A483A1254AF3AEEC CRC64;
 SEQUENCE FROM N.A.
MEDLINE=97480713; PubMed=9339358;
Hagg P.M., Horelli-Kuitunen N., Eklund L., Palotie A.,
 Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 PRT; 1367 AA
 Created)
 Created)
 01-JAN-1998 (TrEMBLrel. 05, C: 01-JAN-1998 (TrEMBLrel. 05, Lk 01-OCT-2003 (TrEMBLrel. 25, Lk Type XV collagen.
 Q9EQD9;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
Type XV collagen.
 PRELIMINARY;
 181 SFSK 184
 358 QSKK 361
 Collagen.
SEQUENCE
 035206
 Q9EQD9
 RESULT 13
Q9EQD9
ID Q9EQD
AC Q9EQD
DT 01-MADT 01-MC
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 1183
 61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW 120
 121 HGSDPSGRRITDSYCETWRIEAFAATGGASSLIAGRILEGEAASCRHAFVVICIENSVWT 180
 "Cloning of three variants of type XVIII collagen and their expression patterns during Xenopus laevis development.";

Mech. Dev. 114:109-113(2002).

EMBL; AX052763; AAL1457.1; -..
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR008160; Collagen.
InterPro; IPR001129; TSPN.
Pfam; PF01210; TSPN; 1.
 61 VRRADRIGVPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVW
 121 HGSDPSGRRITDSYCETWRIEAPATGQASSLLAGRLIEQEAASCRHAFVVICIENSVMT
 1 HTHQDFQLVLHLVALNSPQPGGNRGIRGADFQCFQQARAAGLAGTFRAFLSSRLQDLYSI
 1 HTHODPQLVLHLVALNSPQPGGMRGIRGADFQCPQQARAAGLAGTFRAFLSSRLQDLYSI
 Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
 SEQUENCE FROM N.A.

Haftek Z., Morvan-Dubois G., Thisse B., Garrone R., Le Guellec D.;

"Sequence and embryonic expression of collagen XVIII NCII domain
(endostatin) in the zebrafish.";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ494837; CAD38825.1;

NON TER
 65.2%; Score 631.5; DB 13; Length 361; 65.2%; Pred. No. 3.7e-55; Live 22; Mismatches 41; Indels 1;
 71.5%; Score 691; DB 13; Length 1307; 70.1%; Pred. No. 1.9e-60; ive 18; Mismatches 37; Indels 0;
 1307 AA; 134153 MW; D53EDBFE3DE34976 CRC64;
 SEQUENCE 361 AA; 40222 MW; 3C5A0F8479D26735 CRC64;
 01-MAR.2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Collagen XVIII (Fragment).
 361 AA.
 Query Match
Best Local Similarity 70.1%
Matches 129; Conservative
 Query Match
Best Local Similarity 65.2%
Matches 120; Conservative
 SMART; SM00210; TSPN; 1.
Collagen.
SEQUENCE 1307 AA; 134:
 PRELIMINARY;
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1304 NNRK 1307
 181 SFSK 184
 QBAWC6
 RESULT 11
Q8AWC6
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Type XV collagen.
 NCBI_TaxID = 9606;
 LISAL
 Q9Y4W4
 Q9Y4W4
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 69 VPVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWPRKSVWHGSDPSGR 128
 9 VIHIVALNSPOPGGMRGIRGADFOCFOOARAAGIAGTFRAFISSRIODLYSIVRRADRIG 68
 STRAIN=129/Sv, MEDLINE=20522048; PubMed=11068203; MEDLINE=20522048; PubMed=11068203; MEDLINE=20522048; Fallond L., Muona A., Lietard J., Pihlajaniemi T.; Structure of the mouse type XV collagen gene, Coll5al, comparison with the human Coll5Al gene and functional analysis of the promoters of both genes.";
 Pihlajaniemi T.; Cloring of mouse type XV collagen sequences and mapping of the corresponding gene to 481-3. Comparison of mouse and human alpha 1 (XV) collagen sequences indicates divergence in the number of small collagenous domains."; Genomics 45:31-41(1997).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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 GO; GO: 0007155; F: Erructural molecule activity; IEA. GO; GO: 0007155; P: Cell adhesion; IEA. InterPro; IPR008161; Clg_helix.
InterPro; IPR008161; Colgaen.
InterPro; IPR008985; Cond_like_lec_gl.
InterPro; IPR001791; Laminin_G.
InterPro; IPR0013129; TSPN.
Pfam; PF01391; Collagen; P.
Propom; PF0210; TSPN; 1.
Propom; PF0210; TSPN; 1.
SWART; SM00282; Lamig; 1.
 MEDLINE=97480713, PubMed=9339388,
Hagg P.M., Horelli-Kuitunen N., Eklund L., Palotie A.,
 MALLIX BJO1. 19:489-500(2000),
EMBL, APS61101, AAG27451;
EMBL, APS61101, AAG27451;
EMBL, APS61101, AAG27451;
EMBL, APS61111, AAG27451;
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EMBL, APS6
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Matches
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RAY PEQUENCE FROM N.A.

RX MEDINES 28016557; PubMed=9651385;
REDINES 28016557; PubMed=9651385;
RT MEDINES 28016557; PubMed=9651385;
RT Complete exon-intron organization of the human gene for the alphal cromparts of the comparison with the homologous RT COLISIN Of the human gene for the alphal cromparison of type XV collagen (COLISAL) and comparison with the homologous RT COLISIN Office.

REDIN 125280; AAC78800.1; OINED.

REDIN 125280; AAC78800.1; OINED.

REDIN 125285380; AAC78800.1; OINED.

REDIN 125285380; AAC78800.1; OINED.

REDIN 12528596; AAC78800.1; OINED.

REDIN 125286; AAC78800.1; OINED.

REDIN 125289; A
 1312 RLVDKYCEAMRTTDMAVTGFASPLSTGKILDQKAYSCANRLIVLCIENSFMTDTRK 1367
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MEDINE=54149820; PubMed=8106446;
MEDINE=54149820; PubMed=8106446;
MINITAIRNO S., Heinamaki P., Rehn M., Honkanen N., Myers J.C.,
Pihlajaniemi T.;
Pirliary Structure of the alpha 1 chain of human type XV collagen and
Exon-infron organization in the 3' region of the corresponding gene.",
J. Biol. Chem. 269:4773-4779(1994).
129 RIIDSYCETWRIEAPAATGQASSILAGRLLEQEAASCRHAFVVLCIENSVMISFSK 184
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Last sequence update)
Last annotation update)
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 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25,
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67 TGVPVVNLRDEVLFPSWEALFSGSEGOLKPGARIFSFDGRDVLOHPAWPRKSVWHGSDPS 126
 PVVNLRDEVLFPSWEALFSGSEGQLKPGARIFSFDGRDVLQHPAWFRKSVWHGSDPSGRR 129
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 10 LHLVALNSPOPGGWRGIRGADFOCFQOARAAGLAGTFRAFLSSRLQDLYSIVRRADRIGV 69
 1; Gaps
 4; Gaps
 130 LIDSYCETWRIEAPAATGOASSLLAGRLLEGEAASCRHAFVVLCIENSVMISFSK 184
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 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
NCBI_TaxID=7719;
 SEQUENCE FROM N.A.
Hotta K., Takahashi H., Satoh N.;
"Further Characterization of Brachyury-Downstream Genes in Ciona
 47.4%; Score 457.5; DB 5; Length 950; 55.2%; Pred. No. 4.2e-37; tive 17; Mismatches 60; Indels 1
 Length 1388;
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54.6%; Score 527; DB 4; Length 13

Best Local Similarity 56.6%; Pred. No. 6.8e-44;

Matches 99; Conservative 27; Mismatches 45; Indels
 intestinalis Embryo.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB076899 BAC57521.1;
InterPro; IPR00160; Collagen.
InterPro; IPR001759; Pentaxin.
Pfam; PF01391; Collagen.
PROSTIE: PS00289; PRNTAXIN; 1.
SEQUENCE 950 AA; 94768 MW; 2767ECA158CBA89F CRC64;
 Collagen.
SEQUENCE 1388 AA; 141757 MW; 96828E45E847194B CRC64;
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Last annotation update)
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 Query Match
Best Local Similarity
Matches 96; Conservat
 Ciona intestinalis.
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